Scoring table:

Total number

score:

Perfect

Sequence:

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Human pep
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Human ext
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Anglogene
Mrg precu
Human meg
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Novel hum
Human tes
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Human pro
Pseudomon
Human ORF
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Novel hum
Antheraea
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Pseudomon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; proliferation differentiation factor; haematopoietic function.
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                                   Abg35520 Abd5409 Abd5409 Abd55409 Abd55409 Abu55525 Abd67911 Abd67912 Abd67912 Abd66919 Abd6797 Abd67
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ABP64957
ABO69289
AAB43375
ABO73785
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ABJ18375
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AAR26049
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N-PSDB; AAF29348.
WO200104312-A1
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18-OCT-1999;
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-MODEL=frame+ n. del -DEV=xlp
-MODEL=frame+ n. del -DEV=xlp
-MODEL=frame+ n. del -DEV=xlp
-MODEL=frame+ n. del -DEV=xlp
-D=/CGPLZ_1/USPTO_Spool_p/US10030225/runat_18022005_095900_16266/app_query.fasta_1.775
-D=, GGD=2_1/USPTO_Spool_p/US10030225/runat_18022005_095900_1626/app_query.fasta_1.775
-D=, GGD=EXT=0 -UNITS=bits -START=1 -END=-1 -NATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MINS=0 -AMXLEN=15
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLEN=200000000
-USRE=US10030225_GCGN 1 1 224 @runat_18022005_095900_16266 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -MAXT=DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XCAPOP=10 -XCAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOREXT=7
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Aab88193 Human mem
Aam13752 Peptide #
Abb32685 Peptide #
Aam26150 Peptide #
Abb27526 Human pep
Abb18176 Protein #
Aam65885 Human bon
Aam65885 Human bon
Aam65895 Human bon
                                                                                                                                                                                                                            February 18, 2005, 23:59:55; Search time 133.5 Seconds (without alignments) 3702.470 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                       1163
l atgogtgogotcogogacog.....ataaccaggtgaccatcaag 639
                                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                   protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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ABB32685
AAM26150
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AAM65885
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Ygapext
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4: geneseqD2001s:*
5: geneseqD2013s:*
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Match
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Database

11115 430 430 430 430 430 430 430

1084597861

Result

(first entry)

99JP-00194179

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Human, secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes.
                Human membrane or secretory protein clone PSEC0137.
                                                                                                                                           11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766
                                                                                                                 07-JUL-2000; 2000EP-00114090
                                                              Homo sapiens.
                                                                                EP1067182-A2
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23-MAY-2001
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                This invention relates to polynucleotide sequence PSEC137, which encodes a human proliferation differentiation factor protein. Included in the invention is a vector containing the cDNA sequence, a transformant containing the vector, and a process for producing the protein. The protein together with its encoded DNA and antisense DNA are used in drugs to maintain the haematopoietic function. The present sequence represents the human proliferation differentiation factor protein amino acid
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                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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  Claim 1; Page 42-44; 49pp; Japanese
                                                                                                                              7.26e-85
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This invention relates to nucleic acid sequences AAF93744 - AAF93916

which encode human secretory or membrane proteins represented by AAB88317

- AAB88419. Included in the invention are primers AAF93917 - AAF894295 and

- AAB86419. Included in the invention are primers AAF93917 - AAF894295 and

AAF86232 - AAF62235 which are used to isolate the CDNA sequences of the

continuon. The invention also includes methods for the production of

antibodies directed against the proteins, and CDNA sequences. Which can

continuon. The polymucleotide sequences can be used in gene

therapy. The polymucleotide sequences and the proteins they encode may be

the prevention, treatment and diagnosis of diseases associated

with inappropriate secretory protein/membrane protein expression. The

cucleic acids and complementary sequences may also be used as DNA probes

in diagnostic assays (e.g. polymerase chain reactions (FCR)) to detect

and quantitate the presence of similar nucleic acid sequences in samples.

Conteins/membrane polypeptides and their role in metabolism. The

proteins/membrane polypeptides and their role in metabolism. The

control of expression and activity. The antibodies and antagonists

contained antibodies may also be used as therapeutic agents to down regulate expression and

contained the presence of the polypeptides in samples

contained the presence of the polypeptides in samples

contained immunosorbant assay (ELISA). Examples of diseases which may be

contained include rheumatoid arthritis and diabetes
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                                                                                                                                                                                         Nucleic acids encoding secretory proteins/membrane proteins, usefigene therapy or as candidate target molecules in drug development
                                                     Hayashi
                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 154; 609pp + Sequence Listing; English.
                                                     Sugiyama T,
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AAB88393 standard; protein; 571 AA

AAB88393

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                                                                                                   Sequence 81 AA;
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                                     TGGACTGTCACTGAGCCAGCCATGACCCCAGGCAACACCCCTCCCAGGACCCCA 300
                   TGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCAGGACC
LeuGluAlaAlaLeuGlyLeuProValLysLysProArgLeuArgGlyProArgProGly
                                                                                                                AGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGAA
                                                                                                                                                                                                                                                                                             Peptide #186 encoded by probe for measuring cervical gene expression
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2000US-00632366.
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26-MAY-2000; 2
30-JUN-2000; 2
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21-SEP-2000; 2
27-SEP-2000; 2
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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                      The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                        gene expression in human cervical epithelial cells
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Conservative:
Mismatches:
Indels:
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                                                                           Claim 27; SEQ ID NO 18578; 487pp; English
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26-WAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
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Best Local Similarity:
Query Match:
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Chen W,

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04-FEB-2000; 2000US-0180312P.
26-MX-2000; 2000US-0201456P.
30-UJN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-0033266.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023458P.
04-OCT-2000; 2000US-023458P.
                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                 30-JAN-2001; 2001WO-US000663
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                                                                                                                                                                                  The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and singlaplaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                       1 genome-derived single exon nucleic acid probes useful for analyzing expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGGAGGAGGAACCACTGCTCCCC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #187 encoded by probe for measuring placental gene expression.
                                                                                                                                                             Claim 27; SEQ ID NO 25320; 639pp + Sequence Listing; English.
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Matches:
Conservative:
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Indels:
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                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                  Chen W,
27-SEP-2000; 2000US-0236359P. 04-OCT-2000; 2000GB-00024263.
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430.00
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                                                                                            WPI; 2001-483447/52
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Query Match:
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                                                                                                                                                                                                                                                                                                                 Sequence 81 AA;
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                                                                  Penn SG,
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                                                                                                                       Human
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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see AA131315-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGCACCACTGCTCCCC 201
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Mismatches:
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Matches:
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                                                                gene expression in human placenta.
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21355-ABA41365). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                   Protein #175 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
Human, gene expression, heart, microarray, vascular system,
cardiovascular disease, hypertension, cardiac arrhythmia;
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Mismatches:
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Matches:
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                                                                                                                                                                                                ABB18176 standard; protein; 81 AA.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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26-MAY-2000; 2000US-0207456P.
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                                                                                                                                                                                                                                                                                                                                                                                                                        congenital heart disease.
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                                                                  382 CAG 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from wRNA of human breast, and then measuring the label bound to each probes of the microarray. The probes are useful for verifying the propession of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New spatially-addressable set of single exon nucleic acid probes, for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
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2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                         Homo sapiens.
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   201
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                    ArgThrHisLeuGlnAlaGluProHisGlpHisGlyCysTrpThrValThrGluProAla
                                                                                                                                                                   AlaMetThrProGlyAsnAlaThrProProArgThrProGluValThrProLeuArgLeu
                                                                                                                                                                                                                                         GluLeuGlnLysLeuProGlyLeuAlaAsnThrThrLeuSerThrProAsnProAspThr
 GTCTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGCACCACTGCTCCCC
                                                                          AGAACCCACCTGCAGGCAGAGCCACACCAACATGGATGCTGGACTGTCACTGAGCCAGCA
                                                                                                                                                GCCATGACCCCAGGCAACACCACCCCTCCCAGGACCCCCAGAGGTTACTCCGTTGCGGCTG
                                                                                                                                                                                                                      GAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTGAGTACCCCTAACCCTGATACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow expressed probe encoded protein SEQ ID NO: 26191.
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microarray; cancer; leukaemia; lymphoma; myeloma.
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2000US-0234687P.
2000US-0236359P.
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2000US-00608408.
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AAM6588
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81 79

Length: Matches: Conservative:

1.45e-27 430.00 98.77%

Pred. No.: Score: Percent Similarity:

Alignment Scores

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321
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                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human brain expressed single exon probe encoded protein SEQ ID NO: 25612.
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Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy, cancer.
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                                                                                                                                                             41 AlaMetThrProGlyAsnAlaThrProProArgThrProGluValThrProLeuArgLeu
                                                                                                                                                                                                                                                                              GTCTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGAGGCACCACTGCTCCCC
                                                                                                       GAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTGAGTACCCCTAACCCTGATACC
                                                                                                                                              202 AGAACCCACCTGCAGGCAGAGCCACACCAACATGGATGCTGGACTGTCACTGAGCCAGCA
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Mismatches:
Indels:
                                                         US-10-030-225-1_COPY_58_696 (1-639) x AAM65885
                              Gaps:
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0235359P.
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27-SEP-2000; 2
04-OCT-2000; 2
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03-AUG-2000;
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Percent Similarity:
Best Local Similarity:
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                                                                                                             Sequence 81 AA;
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Pred. No.:
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                                                                                                                                     21 ArgThrHisLeuGlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAla 40
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                                                                                                      GAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTGAGTACCCCTAACCCTGATACC
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                                                                                                                            AGAACCCACCTGCAGGCAAGCCACACCAACATGGATGCTGGACTGTCACTGAGCCAGCA
                                                                                                                                                         GCCATGACCCCAGGCAACACCACCCCTCCCAGGGACCCCCAGAGGTTACTCCGTTGCGGCTG
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1 1 1 0 0 0 0 0
                            Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                               US-10-030-225-1_COPY_58_696 (1-639)
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
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                                          Percent Similarity:
Best Local Similarity:
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       Sequence 81 AA
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosts, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ValSerAlaSerProAspProArgProLeuLysGluGluGluGluAlaProLeuLeuPro
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Mismatches:
Indels:
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Matches:
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532566.
21-SEP-2000; 2000US-0234687P.
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The present invention relates to novel single exon nucleic acid probes (see AAI00010-AAI10067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast diseases and non-carcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                             Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human peptide encoded by genome-derived single exon probe SEQ ID 25185,
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Mismatches:
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Matches:
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                                                                               Chen W, Rank DR;
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                                               (MOLE-) MOLECULAR DYNAMICS INC.
               04-OCT-2000; 2000GB-00024263.
27-SEP-2000; 2000US-0236359P.
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                                                                               Penn SG, Hanzel DK,
                                                                                                             WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                human breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 81 AA;
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The invention relates to a spatially-addressable set of single exon mucleic acid probes for measuring gene expression in a sample derived from the card probes for measuring gene expression in a sample derived from the comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their probes. Also included are a microarray comprising the novel set of probes which phybridises at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a sample cit derived from human lung massuring the label detectably bound to each probe of the array, identifying exons in a ewkaryote genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the ewaryote and (b) measuring the label detectably bound to each probe of the array identically predicting at least one exon from genomic sequences of the advance; and (b) detecting specific hybridiastion of algorithmically predicting to the predicted exon, the probe is included a labeled nucleic acids from ewkaryote lung mRNA, to a single exon probe having a fragment identical to the predicted exon, the probe is included the above mentioned microarray; assigning exons to a single exon probe having a fragment identifying exons from genomic sequence by the method expression of the exons in the tissues and/or cell types undicates that the exons about do a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types undicates that the exons about do a single gene, a peptide comprising on the exons in the tissues and/or cell types used for identifying exons in a gene particularly using human lung derived mRNA and for the exons in a gene patted for derivity of malysis, and for identifying exons in a periode for gene expression of the exons solerosis, landmonary disease (IDD), interstitial lung cancer, chronic obstructive
                    Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary histiocytosis; Iymphangioleiomyomtosis; Karagener syndrome; pulmonary hveolar proteinosis; fibrocystic pulmonary dysplasia; purary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 27; SEQ ID NO 25185; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                       03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                2000US-0207456P.
2000US-00608408.
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                                                                                                                                                                                                                                                                                                                            2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-114183/15.
                                                                                                                                                                                              WO200186003-A2.
                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
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                                                                                                                                                                                                                                         15-NOV-2001
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engineered to comprise (I) which is operatively associated with a
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                                                                                                                                        261
                                                                                                                                                                          GCCATGACCCCAGGCAACACCACCCCTCCCAGGACCCCCAGGGTTACTCCGTTGCGGCTG 321
                                                                                                                                                                                                             GAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTGAGTACCCCTAACCCTGATACC 381
                                                                                                                                                                                                                                                                                                                                                                      biological activity; genetic engineering; hybridisation probe; oligomer; primer; chromosome mapping; gene mapping; recombinant protein production; human.
                                                                                                               New polynucleotides, useful as hybridization probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                                                                                                                                                                                                                      142 GTCTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGAGGCACCACTGCTCCCC
                                                                                                                                         AGAACCCACCTGCAGGCAGAGCCACACCACATGGATGCTGGACTGTCACTGAGCCAGCA
                          4874400
                         Length:
Matches:
Conservative:
Mismatches:
                                                                                     US-10-030-225-1_COPY_58_696 (1-639) x ABG35520 (1-81)
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                                                                                                                                                                                                                                                                                                                                                       Human polypeptide sequence SEQ ID NO:1817.
                                                            Indels:
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                                                                                                                                                                                                                                                                                                    ADF59409 standard; protein; 173 AA
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                         1.45e-27
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                                430.00
98.77%
97.53%
36.97%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-876918/81.
                                         Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                CAG 384
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Sequence 81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                Alignment Scores:
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regulatory sequence that modulates expression of (I) in the host cell; (4) a polypeptide (II) encoded by (I); (5) a composition comprising the polypeptide of (4) and a carrier; (6) an antibody directed against the polypeptide of (4); (7) detecting (I) or the polypeptide of (4) in a sample; (8) identifying a compound that binds to the polypeptide of (4); (9) producing the polypeptide of (4); and (10) a collection of polynucleotides comprising at least one of the polynucleotide sequences (I). The polynucleotides (I) can be used as hybridisation probes, oligomers or primers, for chromosome or gene mapping, for the recombinant production of proteins, and for generating antisense DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CTGGAGGCGCGCTAAGGCTCCCCGTGAAGAAGCCGCGGCTCCGCGGACCACGGCCTGGG 120
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-----ThrGlyMetArgProGlySerLeuAlaAla 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229 CAACATGGATGCTGGACTGTCACTGAGCCAGCAGCCATGACCCCCAGGCAACACCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCGTGCGCTCCGCGACCGAGCGGGCTCCTCCTCTGCGTGCTGCTGCTGGCGGCGCTG
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59
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Matches:
Conservative:
Mismatches:
Indels:
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230.00
56.03%
50.86%
19.78%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                Sequence 173 AA;
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ABU53252 standard; protein; 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                18970 SerProGlyThrProSerSerArgProSerProThrCysProSerAlaAlaAlaAraThr 18989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TrpArg-- 19084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19049 ----------SerSerThrSerSerProProValArgProSerProAr 19061
                                                                                                                    The invention relates to avilamycin derivatives (1) with antibacterial, vibucide, protozoacide and fundicide activity. (1) are useful for treatment of infections (bacterial, viral, protozoal or fungal), in human or veterinary medicine, particularly where caused by Staphylococcus aucusus. (1) are more hydrophilic than known avilamycins. The present sequence is that of an avilamycin synthesis enzyme from the Streptomyces viridochromogenes Avilamycin pynthetic gene cluster (ABZ37515-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 GAAGAAGCCGCGGCTCCGCGGACCACGCCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 AGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGACCACCACTGCTCCCCAGAAC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                           86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 ACGACTGCTCCCCAGAACCCACCTGCAGGCAGAGCTACACCAACATGGATGTTGGACTGT
                                                          New avilamycin derivatives, useful for treatment of infections, and nucleic acid encoding avilamycin synthesis enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTGAGCCAGCACCCTGACCCCAGGGAATGCCACGCCTCCCAGG 537
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Bechthold A;
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Conservative:
Mismatches:
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 Trefzer A,
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                                                                                             Example 1; Page 68-301; 319pp; German.
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Muehlenweg A,
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                                                                                                                                                                                                                                                                            154.00
33.16%
27.04%
13.24%
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                       2003-018650/01.
B; ABZ37515.
                                                                                                                                                                                                                               Sequence 19938 AA;
                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
 Weitnauer G,
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ABU53252
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from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 GCAGGCAGACCACACCACACATGCTGGACTGTCACTGAGCCAGCAGCATGACC-- 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 proAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.
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                                                                                                                         Human; gene therapy; vaccine; disease treatment; detection.
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                                                            Human testes-derived DKFZphtes3_4019 homologue #1
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEHU-) GERMAN HUMAN GENOME PROJECT.
                                                                                                                                                                                                                                                                                                                                                                             18-AUG-2000; 2000WO-IB001496.
                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0149499P
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Best Local Similarity:
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                                                                                                                                                                                                                                                   WO200112659-A2.
                                                                                                                                                                                         Homo sapiens
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14-APR-2003
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468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCTGACC------CCAGG 518
                                                                                                                                                                                                                                                                                                                                                              190 oLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAl 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                        210 aProThrThrProLysGluThrAlaProThrThrProLysGlyThrAlaProThrThrLe 230
90 aProThrThrProLysGluProAlaProThrThrProLysGluProAlaProThrThrTh 110
                                     -----CCAGGCAACACCACCCTCCCAGGACCCC 299
                                                            300 AGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTT 359
                                                                                                                                                                                360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA------GATCCTAG 407
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Search completed: February 19, 2005, 00:16:30 Job time : 152.5 secs

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Sequence 18035, A Sequence 2531, A Sequence 20281, A Sequence 24221, A Sequence 2421, A Sequence 10, Appl Sequence 11, Appl Sequence 147, Appl Sequence 47, Appl Sequence 147, Appl Sequence 1845, A Sequence 18845, A Sequence 26099, A Sequence 26099, A
                    Sequence 40, Appl
Sequence 2, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 18, Appl
Sequence 1, Appl
Sequence 1, Appl
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Sequence 8970, Ap
Sequence 26135, A
Sequence 31529, A
Patent No. 5168049
Patent No. 5168049
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Sequence 11715,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF NIVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAM-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
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US-07-757-022B-62
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US-09-299-970A-1
US-09-552-991A-18035
US-09-252-991A-2553
US-09-252-991A-2253
US-09-252-991A-2421
US-09-252-991A-2591
US-09-252-991A-2591
US-09-252-991A-2591
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US-09-894-998A-47
US-10-237-551-47
US-09-252-991A-19845
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US-09-616-289-47
US-09-949-016-11716
US-09-252-991A-30843
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3-07-757-022B-52
3-07-757-022B-2
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; Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WALT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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44, Appl
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142, App
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(without alignments)
3028.619 Million cell updates/sec
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. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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. /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                             protein search, using frame plus n2p model
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US-07-757-022B-84
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US-07-757-022B-104
US-07-757-022B-104
US-07-757-022B-42
US-07-757-022B-42
US-07-757-022B-45
US-07-757-022B-46
US-07-757-022B-60
US-07-757-022B-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                               US-10-030-225-1_COPY_58_696
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match
                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Perfect score:
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Maximum DB seq
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Jatabase :

Result

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380 ProAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 399
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                                                                                                                                                                                                                                                                                                                                    Megakaryocyte Stimulating Factors
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124
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  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gener. Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
ITILE OF INVENTION: Megakaryocyte Stimu.
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION UNBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: US 07/390,901
FILING DATE: US 07/390,901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        Sequence 84, Application US/07757022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 84:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.35e-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
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Best Local Similarity:
                                                                                                                                                                  ; Patent No. 6433142
                                                                                        RESULT 2
US-07-757-022B-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-757-022B-84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18
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DB:
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Matches:
Conservative:
Mismatches:
Indels:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUARN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
TELEPAX: (617)876-1170
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148.50
32.48%
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
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                                                       400 ThrProLysGluProAlaProThrThrLysSerAlaProThrThrLysGluPro 419
                                                                                                  153 CCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGCACCACACTGCTCCCCAGAACCCACT 212
                                                                                                                                                                         213 GCAGGCAGACCACCAACATGGATGCTGGACTGTCACTGAGCCAGCAGCCATGACC-- 270
                                                                                                                                                                                                                                             ---CCAGGCAACACCACCCCTCCCAGGACCCC 299
                                                                                                                                                                                                                                                                             479 rLysLysProAlaProThrAlaProLysGluProAlaProThrThrProLysGluThrAl 499
                                                                                                                                                                                                                                                                                                              300 AGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTT 359
                                                                                                                                                                                                                                                                                                                                                                                    ---GATCCTAG 407
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                                  GCTCCGCGCACCACGCCTGGGAGCTCACGAGGCTCGCAGAGGTCTCA-----GCCTC 152
                                                                                                                                                                                                       459 aProThrThrProLysGluProAlaProThrThrProLysGluProAlaProThrThrTh 479
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                                                                                                                                                                                                                                                                                                                                                                                GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA-
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87 CambridgePark Drive
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 74, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: GESNEY, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Geener, Thomas G. APPLICANT: Clark, Srephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryc
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STATE: Massachusetts
COUNTRY: U.S.A.
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ADDRESSEE: Genetics
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GCTCCGCGGACCACGGCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTCA-----GCCTC 152
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64
12
124
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Matches:
Conservative:
Mismatches:
Indels:
                                                                         FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: ANG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUMBIN
                                                              US 07/457,196
                                                                                                                                                                                                    RECISTATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 GCTCCCCGTGAAGAAGCC--
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32.48%
27.35%
12.77%
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
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Best Local Similarity:
Query Match:
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606 aProThrihrbroLysGluihrAlaProThrihrbroLysGlyThrAlaProThrThrLe 626
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                                                                                                                                                                                                      153 CCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGCACCACTGCTCCCCAGAACCCACT 212
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GCTCCGCGGACCACGCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTCA-----GCCTC 152
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466 rLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysLysProAl 486
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                                                                                         127 ThrProLysGluProAlaProThrThrThrLysSerAlaProThrThrThrLysGluPro
                                                                                                                                                                   447 AlabronhrhhrhriysSerAlabro-thrnhrProLysGluProSerProThrThr
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                                                              78 GCTCCCCGTGAAGAAGCC
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US-07-757-022B-104
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STREET: 87
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                                            563 aProThrThrbroLysGluThrAlaProThrThrProLysGlyThrAlaProThrThrLe 583
         519 GAATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGCTGGAGCTGCAGAAGCT
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                                                                                                                                                                                                                                                  APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                     GCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT 618
                                                                                                                        583 uLysGluProAlaProThrThrProLysLysProAlaPro 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PEPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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Mismatches:
Indels:
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Matches:
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APPLICATION NUMBER: US 07/546,114
FILIND DATE: 29-UUN-1990
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILIND DATE: 29-DEC-1989
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILIND DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UMBER: US 07/643,502
18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                  US-07-757-022B-58
; Sequence 58, Application US/07757022B
Patent No. 6433142
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     E: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 0.5.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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APPLICATION NUMBER:
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DB:
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Sequence 104, Application US/07757022B

Patent No. 643142

GENERAL INFORMATION:

APPLICANT: Genner, Thomas G.

APPLICANT: Turner, Katherine

APPLICANT: Hewick, Rodiney M.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Floppy Misk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                            Inc.
                                                                                                                                                                                                                                                                                            E: Genetics Institute,
87 CambridgePark Drive
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----CCAGG 518
                                                                                                                                                        697 aProThrThrProLysGluThrAlaProThrThrProLysGlyThrAlaProThrThrLe 717
                                                                   677 oLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAl 697
                                                                                                               519 GAATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGCTGGAGCTGCAGAAGCT
                         468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC
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143
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                                                                                                                                                                                                    579 GCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910 CLASSIFICATION: 530
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Matches:
Conservative:
Mismatches:
Indels:
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FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION UNBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETT, LUADIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                 Sequence 44, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Scephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION TELECOMMUNICATION: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                               US-07-757-022B-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCCGCGGACCACGGCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTCA-----GCCTC 152
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNA-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                          NAME: CBERT, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
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148.50
32.48%
27.35%
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TOPOLOGY:
SOFTWARE
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                                                                                                                                                                                                                                                                                                                                                                                                           300 AGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                      aProThrThrProLysLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GATCCTAG 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                884 ThrProLysGluProAlaProThrThrLysSerAlaProThrThrLysGluPro 403
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                                                                                                                                                                                                                             CCCAGATCCTAGGCCTCTGAAGGAAGGAGGAGGCACCACTGCTCCCCAGAACCCACT 212
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                                                                         ProAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 383
                                               CCGAGCCGGGCTCCTCTGCTGCTGCTGCTGCGGGCGCTGCTGGAGGCGGCGCTTAGG 77
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                                                                                                                                                                   GCTCCGCGCACCACGGCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTCA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468 ACACCAACATGATGTTGGACTGTCACTGAGCCAGCCCTGACC----
               US-10-030-225-1_COPY_58_696 (1-639) x US-07-757-022B-44 (1-1270)
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                                                                                                          78 GCTCCCCGTGAAGAAGCC-------
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87 CambridgePark Drive
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; Sequence 42, Application US/07757022B
; Patent No. 6433142
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CITY: Cambridge
STATE: Massachusetts
COUNTX: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Geener, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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PatentIn Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
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                                                                                                                                    PILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
PILING DATE: 29-UNN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
                                  APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
                                                                                               RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
PILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                             US 07/390,901
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION:
TELECOMMUNICATION: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1311 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0'
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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32.48%
27.35%
12.77%
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INFORMATION FOR SEQ ID NO:
                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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TELEFAX: (
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Percent Similarity:
Best Local Similarity:
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544 oGluLysProAlaProThrThrProGluGluLeuAlaProThrThrProGluGluProTh 564
                                 564 rProThrThrProGluGluProAlaProThrThrProLysAlaAlaAlaProAsnThrPr 584
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                                                                                                   468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC----
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APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Thurner, Katherine
APPLICANT: Thurner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                     GCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT 618
                                                                                                                                                                                                                                                                      624 uLysGluProAlaProThrThrProLysLysProAlaPro 637
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING PATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICKTION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     US-07-757-022B-142
; Sequence 142, Application US/07757022B
; Patent No. 6433142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 142: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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MEDIUM TYPE: Floppy
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TYPE: AMINO ACID
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Alignment Scores:

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                                                                                                                                                                                                               519 GAATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGCTGGAGGCTGCAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC----
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                     Gaps:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/07757022B
Fatent No. 6431142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte St
  9.87e-05
148.50
32.48%
27.35%
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STATE: Massachu
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Sequence 46, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: AMINO ACID
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STATE: Massachue
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CLASSIFICATION:
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                                                                                                           Patentin Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETY, LUADIN
                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CEET, LUADN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION
TELEPHONE: (617)876-1170
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SEQUENCE CHARACTERISTICS:
LENGTH: 1314 amino acids
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27.35%
12.77%
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Best Local Similarity:
Query Match:
U.S.A
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Pred. No.:
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468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC-----CCAGG 518
                                                                            ------GATCCTAG 407
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                                                                          360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA-
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
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ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
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INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
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148.50
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AMINO ACID
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                                                                       Massachusetts
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CORRESPONDENCE ADDRESS:
                                                   Cambridge
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Best Local Similarity:
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573 rProThrThrProGluGluProAlaProThrThrProLysAlaAlaAlaProAsnThrPr 593
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|134 ThrProLysGluProAlaProThrThrThrLysSerAlaProThrThrLysGluPro 453
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                                                                                                                                                                                                                                                                                                                           GCTCCCCGTGAAGAAGCC----GCG 98
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Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Genner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Hewick, Ratherine
APPLICANT: Hewisch, Ratherine
APPLICANT: Hewisch, Ratherine
APPLICANT: Hewisch, Ratherine
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                                                                                                                        Conservative:
Mismatches:
Indels:
                                                                                      Length:
Matches:
                                                                               9.88e-05
148.50
32.48%
27.35%
               TYPE: protein
                                                                                                                                         Best Local Similarity:
Query Match:
                                                                                                                        Percent Similarity:
TOPOLOGY:
                              US-07-757-022B-46
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                                                                    Alignment Scores:
               MOLECULE
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|ProAlaproThrThrProLysGluProAlaProThrThrLysGluProSerProThr 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysLysProAl 493
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 530
CLASSIFICATION: 530
RELOR APPLICATION NUMBER: 07/643,502
FILING DATE: 18-JAN-1991
RELOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
RELOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
RELOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
Inc.
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Policy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CBELT, LUANN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78 GCTCCCCGTGAAGAAGCC---
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573 rProThrThrProgludluProAlaProThrThrProLysAlaAlaAlaProAsnThrPr 593
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360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA------GATCCTAG
                                                      -----CCAGGCAACACCACCCTCCCAGGACCCC
                                                                                                                            300 AGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCCACACCTT
                                                                                       513 rLysLysProAlaProThrThrProLysGluProAlaProThrThrProLysGluThrAl
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CUBRENT APPLICATION DATA:
BLIANION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 48, Application US/07757022B
Patent No. 643142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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REGISTRATION NUMBER:
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US-07-757-022B-48
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434 ThrProLysGluProAlaProThrThrThrLysSerAlaProThrThrThrLysGluPro 453
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533 aProThrThrProLysLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr
                              513 rLysLysProAlaProThrAlaProLysGluProAlaProThrThrProLysGluThrAl
                                                                                                                                        360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA------GATCCTAG
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Patent No. 6657054
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Regulated Anglogenesis Genes and Polypeptides
FILE REFERENCE: 1U 103 R1
CURRENT APPLICATION NUMBER: US/10/164,595
CURRENT APPLICATION DATE: 2002-06-10
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin version 3.1
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Matches:
Conservative:
Mismatches:
Indels:
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32.48%
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US-10-164-595-58
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Pred. No.:
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Query Match:
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468 ThrProLysGluProAlaProThrThrLysSerAlaProThrThrLysGluPro 487
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Mismatches:
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US-07-757-0228-40
; Sequence 40, Application US/07757022B
REFERENCE/DOCKET NUMBER: GI -
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-581
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acide
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32.48%
27.35%
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                                                                                                                                                      MOLECULE TYPE: protein
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Best Local Similarity:
                                                                                                                                                                         US-07-757-022B-48
                                                                                                                                       TOPOLOGY:
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GCTCCGCGGACCACGGCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTCA-----GCCTC 152
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APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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Matches:
Conservative:
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Indels:
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CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REPERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                               IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 40:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.95e-05
148.50
32.48%
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                                                                                                                                                                                                Cambridge
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: protein
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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Best Local Similarity:
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574 aProThrThrProLysLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr 594
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                                                             GCAGGCAGAGCCACCAACATGGATGCTGGACTGTCACTGAGCCAGCAGCCATGACC-- 270
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CCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGCACCACTGCTCCCCAGAACCCACT
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                                                                                                                          514 rLysGlubroAlaProThrThrProLysGluProAlaProThrThrProLysLysProAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Teark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: DatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/757,022B

FILING DATE: 19910910

CLIASSIFICATION: 530

PLOSSIFICATION: 530

PLOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502

#17,ING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
US-07-757-022B-52
; Sequence 52, Application US/07757022B
; Patent No. 6433142
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64
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                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
US 07/390,901
                                                NAME: CBERT, LUGAN
REGISTATION UNDRER: 31,822
REPERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1363 amino acids
TYPE: AMINO ACID
             FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETT, LUADIN
                                                                                                                                                                                                                                                                                                                       9.95e-05
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32.48%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Search completed: February 19, 2005, 00:24:15 Job time : 45:5 secs

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JAPPLICATT Burgess et al.

APPLICATT BURGESS et al.

TITLE OF INVENTION: No. US20040039163Alel Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-099

CURRENT APPLICATION NUMBER: US/09/939,853A

CURRENT APPLICATION NUMBER: 60/226,191

PRIOR APPLICATION NUMBER: 60/267,300

PRIOR PILING DATE: 2000-08-25

PRIOR FILING DATE: 2001-02-08

PRIOR FILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-20

PRIOR PILING DATE: 2001-03-20

PRIOR PLING DATE: 2001-03-20

NUMBER OF SEQ ID NOS: 159

SOFTWARE: Patentin Ver. 2.1.

SEQ ID NO 94
                                        Sequence 48, Appl
Sequence 40, Appl
Sequence 52, Appl
Sequence 30, Appl
Sequence 1, Appli
Sequence 62, Appli
Sequence 62, Appli
Sequence 55, Appli
Sequence 55, Appli
Sequence 116565,
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Sequence 46, p
Sequence 60, p
Sequence 48, p
Sequence 40, p
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Sequence 4
Sequence 4
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                                           US-09-939-853A-94
US-10-074-978A-403
US-10-10-437-966-13474
US-10-124-557-14
US-10-124-557-14
US-10-124-557-14
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US-10-124-557-16
US-09-807-188-1
US-09-807-188-1
US-10-124-557-65
US-10-124-13-963-11938
US-10-1247-963-11938
US-10-1247-963-11938
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Length
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-WODEL=frame+.ii2p.model -DEV=xlp
-WODEL=frame+.ii2p.model -DEV=xlp
-G-GPIZ 1/USFPTO spool p/US1003025/runat_18022005_095903_16366/app_query.fasta_1.775
-G-CGPIZ 1/USFPTO spool p/US1003025/runat_18022005_095903_16366/app_query.fasta_1.775
-DB-Published Applications AA -OFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOÖPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRAMS=humanq0.cdi -LIST=45 -DOCALIGN=200 -THR MAXED-ECL -THR MAXED
-MAXLEN=2000000000 -USER=US10030225_@CGN 1 1 199 @runat 18022005_095903_16366
-MAXLEN=2000000000 -USER=US10030225_@CGN 1 1 199 @runat 18022005_095903_16366
-LONGLOG - DEV_TIMEOTT=120 -WARN TIMEOUT=30 -THREADT=120 -WARN TIMEOUT=30 -THREADT=120 -WARN TIMEOUT=30 -THREADT=120 -XGAPEXT=0.5
                                                                                                                                                                                February 19, 2005, 00:21:47; Search time 118.5 Seconds (without alignments) 3529.232 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/Der Tewn Publ.pep:*
3: /cgn2_6/ptodata/2/pubpaa/Der Tewn Publ.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USO0_NEW PUB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                  - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1380268 segs, 327241040 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                 US-10-030-225-1_COPY_58_696
                                                                                                                                                                                                                                                                                                                                                                                                                                           , Xgapext
, Ygapext
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Ygapop 10.0 , Y
Fgapop 6.0 , F
Delop 6.0 , D
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Database :

Result

165015, 5, Appli 181500,

201378,

176449,

43328, A 197924, 6, Appli 8, Appli 188969,

145800,

11938, A

Same

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RESULT 2
US-10-074-978A-403
US-10-074-978A-403
Sequence 403, Application US/10074978A
Publication No. US20040010119A1
GENERAL INFORMATION:
APPLICANT: Lette, Markorly A
                                                                                                                                                         Casman, Stacie
Boldog, Ferenc
Patturajan, Meera
Blalock, Angela
Ballinger, Robert
Vernet, Corine
TChernev, Velizar T
Malyankar, Uriel M
Gusev, Vladimir
                                                                                Spytek, Kimberly A
Guo, Xiaojia (Sasha)
Fernandes, Elma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.66e-57
                                                                                                                                                                                                                                                                                                                                                                                                                                   Stone, Dave
Millet, Isabelle
Peyman, John
                                                                                                                                                                                                                                                                Gusev, Vladimir
Rastelli, Luca
Mezes, Peter S
Bllerman, Karen
Heyes, Melvin P
                                                                                                                                                                                                                                                                                                                                                                                                           Edinger, Shlomit
Gunther, Erik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 403
LENGTH: 538
                                                                                                                        Li, Li
Kekuda, Ramesh
Liu, Xiahong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo
US-10-074-978A-403
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Pred. No.:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 GAGCCACACATGGATGCTGGACTGTCACTGAGCCAGCCATGACCCCAGGCAAC 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 AlaGluLeuHisGlnHisGlyCysTrpThrValThrGluProAlaAlaLeuThrProGly 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGATTGGCCAGCACAACCTTGAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA 399
                                                                                                                                                                                                                             CTGGAGGCGGCGTAGGGCTCCCCGTGAAGAAGCCGCGGGCTCCGCGGACCACGGCCTGGG 120
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                                                                                                                                                                                                                                                                               121 AGCCTCACGAGGCTCGCAGAG----- 141
                                                                                                                                                                            ATGCGTGCGCTCCGCGAGCCGGGCTCCTCCTCTGCGTGCTGCTGCTGCTGGCGGCGCTG 60
                                                                                                                                                                                          61 ValProProProGlnProAlaGlySerSerArgAlaGlySerGlyThrGlyThrHisThr 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 GCAGAGCTACAACAACAAGATGTTGGACTGTCACTGAGCCAGCAGCAGCTGACCCCAGGG
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                                                                                                                                                     US-10-030-225-1_COPY_58_696 (1-639) x US-09-939-853A-94 (1-658)
                                                             658
211
                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                              Gaps:
                                                              5.12e-70
1053.50
70.67%
70.33%
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-853A-94
                                                                                                                                                                                                                                                                                                                                        141 -----
                                                                                      Percent Similarity:
Best Local Similarity:
                                                   Alignment Scores:
Pred. No.:
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APPLICANT: PENMAN, JOHN APPLICANT: PENMAN, JOHN APPLICANT: Smithson, Glennda APPLICANT: Smithson, Glennda TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME TITLE REFERENCE: 21402-269
FTILE REFERENCE: 21402-269
CURRENT APPLICATION NUMBER: 60/266,221
PRIOR PLILING DATE: 2001-02-12
PRIOR PLILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-18
PRIOR FILING DATE: 2001-10-19
PRIOR PLILING DATE: 2001-10-19
PRIOR PLILING DATE: 2001-10-19
PRIOR PLILING DATE: 2001-10-14
PRIOR PLILING DATE: 2001-04-02
PRIOR PLILING DATE: 2001-04-02
PRIOR PLILING DATE: 2001-02-14
PRIOR PLILING DATE: 2001-02-14 538 Length: Herrman, John
Pena, Carol B A
Shimkets, Richard A
Taupier Jr, Raymond J
Moore, No. US20040010119A11le
Shenoy, Suresh

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GAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTGAGTACCCCTAACCCTGATACC 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 AlaMetThrProGlyAsnAlaThrProProArgThrProGluValThrProLeuArgLeu
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NY: EXPRESSED IN BT474, SIGNAL = 0.85

NY: EXPRESSED IN BT474, SIGNAL = 0.92

NY: EXPRESSED IN HBL100, SIGNAL = 0.92

NY: EXPRESSED IN HBL100, SIGNAL = 0.92

NY: EXPRESSED IN FETAL LIVER, SIGNAL = 0.95

NY: EXPRESSED IN LUNG, SIGNAL = 0.95

NY: EXPRESSED IN BADUT LIVER, SIGNAL = 0.96

NY: EXPRESSED IN HELA, SIGNAL = 1.4

NY: EXPRESSED IN HELA, SIGNAL = 1.4

NY: EXPRESSED IN HEART, SIGNAL = 1.4

NY: EXPRESSED IN HEART, SIGNAL = 1.4

NY: EXPRESSED IN HEART, SIGNAL = 1.4

NY: EXTRESSED IN HEART, SIGNAL = 1.4
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                                     PRIOR APPLICATION NUMBER: PCT/USUI/00069
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USOI/00668
PRIOR APPLICATION NUMBER: PCT/USOI/00668
PRIOR APPLICATION NUMBER: PCT/USOI/00663
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/USOI/00661
PRIOR PPLICATION NUMBER: PCT/USOI/00661
PRIOR PPLICATION NUMBER: PCT/USOI/00670
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR PLING DATE: 2000-09-21
PRIOR PRIOR DATE: 2000-09-21
PRIOR PRIOR DATE: 2000-09-21
PRIOR PRIOR DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 33474
PLENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                         APPLICATION NUMBER: PCT/US01/00669
FILING DATE: 2001-01-30
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430.00
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97.53%
36.97%
         2001-01-30
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
COTHER INFORMATION:
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Best Local Similarity:
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Sequence 33474, Application US/09864761

Sequence 33474, Application US/09864761

Sequence 33474, Application US/09864761

Sequence 33474, Application US/00864761

Sequence 33474, Application US/00864761

SERENT INCOMPATION: Barron G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hazach, David K.

APPLICANT: Ghan, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FOR ITLE OF INVENTION: HUMBES: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

FRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PELING DATE: 2000-05-26

PRIOR PELING DATE: 2000-06-03

PRIOR PELING DATE: 2000-09-04

PRIOR PELING DATE: 2000-09-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR PELING DATE: 2000-09-04

PRIOR APPLICATION NUMBER: PCT/USO1/00666

PRIOR APPLICATION NUMBER: PCT/USO1/00666

PRIOR APPLICATION NUMBER: PCT/USO1/00667

PRIOR APPLICATION NUMBER: PCT/USO1/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGAGCTGCAGAAGCTGCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCTGAT 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGAAGGAGGAGGAGGACGACTGCTC 441
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                                                                                                                                                                                                             ArgThrHisLeuGlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAla 54
                                                                                                                                                                                                                                                                                                                                                                                        GluLeuGlnLysLeuProGlyLeuAlaAsnThrThrLeuSerThrProAsnProAspThr 94
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       164
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Mismatches:
Indels:
       Matches:
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99.40%
98.80%
75.58%
                       Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                  -----ACCCCTAACCCTGATAACCAGGTG 630
                                                                                                                                                         ACCAACATGGATGTTGGACTGTCACTGAGCCAGCCCTGACCCCCAGGGAATGCCACGC
                                                                                                                                                                                                                        US-10-124-557-14

Sequence 14, Application US/10124557

Publication No. 1002020137894A1

Publication No. 1002020137894A1

CENERAL INFORMATION:

APPLICANT: Turner, Katherine

Clark, Stephen C.

Jacobs, Kenneth

Hewick, Rodney M.

Gener, Thomas G.

TITLE OF INVENTION: Megakaryocyte Stimulating Factors

NUMBER OF SEQUENCES: 143

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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APPLICATION NUMBER: US 07/643,502
PILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
PILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: 31,822
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: amino acid
                                                                                                                                           590 TCCACGCAACCTTGAGT----
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148.50
32.48%
27.35%
12.77%
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Best Local Similarity:
Query Match:
DB:
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                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Road. Thomas J.
APPLICANT: Show, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 196665
LENGTH: 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_92495C.1.pep
US-10-437-963-196665
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Matches:
Conservative:
Mismatches:
Indels:
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OTHER INFORMATION: unsure at all Xaa locations
                                              ; sequence 196665, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
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154.50
41.26%
33.63%
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ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                   300 AGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACCTT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                 418 aProThrThrProLysLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC-----CCAGG 518
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                                                                                                                                                          GCTCCGCGGACCACGGCCTGGGAGCCTCACGAGGCTCGCAGAGGTCTCA-----GCCTC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA-------GATCCTAG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        478 oLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAl 498
                                INVENTION: Megakaryocyte Stimulating Factors
US-10-030-225-1_COPY_58_696 (1-639) x US-10-124-557-14 (1-941)
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 84, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
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COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
                                                                                            GCTCCCCGTGAAGAAGCC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Meg
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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ProAlaProThrThrProLysGluProAlaProThrThrLysGluProSerProThr 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-030-225-1_COPY_58_696 (1-639) x US-10-124-557-84 (1-1022)
Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                               APPLICATION DATE: US 07/643,502
PILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                   NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
                                                                     FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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LENGTH: 1022 amino
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32.48%
27.35%
12.77%
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Best Local Similarity:
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STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                 GCTCCCCGTGAAGAAGCC-
27.35%
12.77%
     Local Similarity:
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                                olysGluProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAl 579
                                                                                                                                     519 GAATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGCTGGAGCTGCAGAAGCT 578
      468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC----
                                                                                                                                                                                                                                                                                                                                                              Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MUTER READABLE FORM:
MUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/W8-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                   599 uLysGluProAlaProThrThrProLysLysProAlaPro 612
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Matches:
Conservative:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5190
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                Sequence 74, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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148.50
32.48%
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Percent Similarity:
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                             US-10-030-225-1_COPY_58_696 (1-639) x US-10-124-557-74 (1-1038)
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Mismatches:
Indels:
Gaps:
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STREET: 87 CambridgePark Drive
CITY: Cambridge
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US-10-124-557-58
Sequence 58, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-124-557-104
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 104, Application US/10124557; Publication No. US20020137894A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Turner, Katherine
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COMPUTER READABLE FORM:
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                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Conservative:
Mismatches:
Indels:
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                                                                                                      APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                           NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEFHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 58: US-10-124-557-58
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                                                                                       CURRENT APPLICATION DATA:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                             PRIOR APPLICATION DATA:
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148.50
32.48%
27.35%
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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Best Local Similarity:
Query Match:
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468 ACACCAACATGGATGTTGGACTGTCACTGAGCCAGCAGCACCTGACC------CCAGG 518
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                                                                                                                                                                                                                                                                                                                                                       606 aProThrThrProLysGluThrAlaProThrThrProLysGlyThrAlaProThrThrLe 626
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Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 uLysGluProAlaProThrThrProLysLysProAlaPro 639
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APPLICATION NUMBER: US 07/546,114
PILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0,
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
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MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25

ZIP: 02140 COMPUTER READABLE FORM:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:

5190

IJ

NAME: Cserr, Luann REGIGSTRATION NUMBER: 31,822 REFERENCE/DOCKET NUMBER: GI TELECOMMUNICATION INFORMATION:

ELEFAX: (617)876-585

TELEPHONE:

INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:

TYPE: amino acid

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212
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                                                                                                             US-10-030-225-1_COPY_58_696 (1-639) x US-10-124-557-104 (1-1140)
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 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                               Gaps:
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148.50
32.48%
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Best Local Similarity:
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US-10-124-557-44
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104 AlabroThrThrLysSerAlaPro-ThrThrProLysGluProSerProThrThrTh 423
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123 ILysGluProAlaProThrThrProLysGluProAlaProThrThrProLysLysProAl 443
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64
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34
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Matches:
Conservative:
Mismatches:
Indels:
                                           NO: 44:
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TOPOLOGY: linear

MOLECULB TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-10-124-557-44
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                                                                                                           0.00949
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32.48%
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                                                                                                                                           Percent Similarity:
Best Local Similarity:
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Sequence 44, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
Clark, Stephen C.
Jacobs, Renneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143

NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
CITY: Cambridge

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| aProThrThrProLysGluProAlaProThrThrTh
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Genner, Thomas G.
TILLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                         1311
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Mismatches:
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Matches:
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Clark, Stephen C.
Jacobs, Kenneth
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27.35%
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Best Local Similarity:
Query Match:
DB:
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                                       Alignment Scores:
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTOR: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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                                   GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
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OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 42:
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42, Application US/10124557
Publication No: US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (617)876-5851
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COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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483
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300 AGAGGTTACTCCGTTGCGGCTGCAGAAGCTGCCGGGATTGGCCAGCACCTT
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0'
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-124-557-50
; Sequence 50, Application US/10124557
; Publication No. US20020137894A1
; GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1314 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Turner, Katherine Clark, Stephen C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (617)876-5851
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STATE: Massachusetts
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|ProAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 426
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 39-DEC-1989
FILING DATE: 08-AUG-1989
Genetics Institute, Inc.
CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
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SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-124-557-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (617)876 - 1170
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                                   CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                       APPLICATION DATA:
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                                                                                         ZIP: 02140
COMPUTER READABLE FORM:
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Best Local Similarity:
Query Match:
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526 aProThrThrProLysLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr
                                                                                                                                                                                               360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA------GATCCTAG
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Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
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FLING DATE: 18-7AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
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FILING DATE: 29-DEC-1989
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REPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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527 aProThrThrProLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr 547
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                                                                                           Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                        Indels:
             MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clark, Stephen C. Jacobs, Kenneth Hewick, Rodney M. Gesner, Thomas G.
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Publication No. US20020137894A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                    US-10-030-225-1 COPY 58 696 (1-639)
                                                                                                         148.50
32.48%
27.35%
12.77%
                                                                                           0.0095
TOPOLOGY: linear
                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                          gnment Scores:
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|ProAlaProThrThrProLysGluProAlaProThrThrLysGluProSerProThr 433
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TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-030-225-1_COPY_58_696 (1-639) x US-10-124-557-46 (1-1320)
                                                                                                                                                                                                                                                                                 Version #1.25
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64
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124
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                   ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                              ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1320 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELEFAX: (617)876-5851
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                                                                                                                             STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 46
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148.50
32.48%
27.35%
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                                                                                                                                                   COUNTRY: U.S.A.
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Best Local Similarity:
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453

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SEQUENCE CHARACTERISTICS
                    LENGTH: 1320 amino
                                   TYPE: amino acid
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533 aProThrThrProLysLeuThrProThrThrProGluLysLeuAlaProThrThrPr 553
--CCAGGCAACACCCCCTCCCAGGACCCC 299
                                                                                                                               ------GATCCTAG 407
                                                                                                                                                                                           593 oLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysGluProAl 613
                                                                                                                                                                                                                                                                                                                                                     613 aProThrThrProLysGluThrAlaProThrThrProLysGlyThrAlaProThrThrLe 633
                                                                                                                                                 rLysLysProAlaProThrAlaProLysGluProAlaProThrThrProLysGluThrAl
                                                               300 AGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACACCTT
                                                                                                                                                                                                                                                         468 ACACCAACATGATGTTGGACTGTCACTGAGCCAGCAGCCCTGACC-----CCAGG
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MEDIUM TYPE: THE COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                     579 GCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT 618
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                                                                                                                             360 GAGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCA-
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Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-UAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/857,196
FILING DATE: 29-DEC-1899
APPLICATION NUMBER: US 07/890,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
TELEPROME: (617)876-5851
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 60, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Turner, Katherine Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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STATE: Massachusetts
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US-10-124-557-60
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||4 ProAlaProThrThrProLysGluProAlaProThrThrThrLysGluProSerProThr 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   513 rLysLysProAlaProThrAlaProLysGluProAlaProThrThrProLysGluThrAl 533
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                                                                                                                                                                                                                                                                                                                                                                        CCGAGCCGGGCTCCTCTCTGCTGCTGCTGCTGGCGCGCTGCTGGAGGCGCGCTAGG 77
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473 rLysGluProAlaProThrThrProLysGluProAlaProThrThrProLysLysProAl
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                                                                                                                                                                                                                                                                                                                       US-10-030-225-1_COPY_58_696 (1-639) x US-10-124-557-60 (1-1320)
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                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                 Indels:
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: February 19, 2005, 00:40:17 Job time : 132.5 secs
                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 GCTCCCGTGAAGAGCC
                                                                                                                                             0.00952
148.50
32.48%
27.35%
                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
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Bassoon protein -immediate-early pr RhoGAP protein [im

hypothetical prote eyelid - fruit fly probable mucin DKF

mucin - rhesus mac apidaecin 73 precu Wiskott-Aldrich sy

hypothetical prote microtubule-associ

sterol regulatory

hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

nascent polypeptid

rotal number

Searched:

mucin 2 precursor, glycoprotein gIII probable multi-dom mucin, submaxillar transactivator EBN

hypothetical prote

hmmediate-early pr

nucleic

Run on:

Sequence:

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A;Cross-references: UNIPROT:Q9GZF7; EMBL:AF067607; PIDN:AAC17641.1; GSPDB:GN00022; CESP:
A;Experimental source: strain Bristol N2; clone C18H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGCTGGAGGGGGCCCCTGTGAAGAAGCGGGGGCTCGGGGACCACGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C18H7.3 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Superfamily: Phaseolus glycine-rich cell wall protein 1.8
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64
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R;Tin-Wollam, A.; Fronick, W.
submitted to the EMBL Data Library, May 1998
A;Description: The sequence of C. elegans cosmid C18H7.
A;Reference number: Z21284
A;Accession: T33110
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                         T31611
T13049
T13049
S35332
3C7807
T21700
S66852
T18311
T19050
T19050
T19050
                                    I49477
T42761
EDBE11
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T29018
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T03099
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A; Residues: 1-460 <TIN>
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Best Local Similarity:
A, Gene: CESP:C18H7.3
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Pred. No.:
                                121
120
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-MODEL=frame+ ni2p.model - DEV=xlp
-MODEL=frame+ ni2p.model - DEV=xlp
-MODEL=frame+ ni2p.model - DEV=xlp
-G=Cgn2 1/USFTO_spool_p/US1003025/runat_18022005_095901_16284/app_query.fasta_1.775
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(c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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Result

Qy 63 GGAGGCGGGGCTAGGGCTCCCCGTGAAGAGCCGCGGGTCCGCGG 107 Db 343 ABGG19SerIleProGlyThrProSerValAlaGInGluSerAlaLyBAlaThrProAla 362 Qy 108 ACCACGGCCTGGG	213 402 273 419 333 357 458 458 458 477	485	Alignment Scores: Pred. No.: Score: 134.00 Matches: 64 Score: 134.00 Matches: 64 Percent Similarity: 34.60% Conservative: 27 Best Local Similarity: 24.33% Mismatches: 109 Query Match: 1.52% Gaps: 10
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each of the twelve author-supplied translations in EMBL: V01555
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A;Rosidues: 1-383 «FRA»
A;Cross-references: UNIPROT:Q04397; UNIPROT:QBAZK8; UNIPROT:QBAZK6; UNIPROT:QBAZK5; UNIF
864.1; PID:g1334836; PID:g1334837; PID:g1334838; PID:g1334839; PID:g1334840; PID:g133484
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NyAlternate names: gene BWRF1 protein
C;Species: human herpesvirus 4, Epstein-Barr virus
C;Date: 13-Jan-1995 #sequence revisite 13-Jan-1995 #text change 09-Jul-2004
C;Accession: S32975; S02383; S32976; S32977; S32978; S32979; S32980; S32981; S32982;
R;Farrell, P.J.
R;Farrell, P.J.
R;Farrell, P.J.
A;Reference number: S32973
A;Accession: S32975
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nThrSerGlnProArgPro-----1leProGlnGlnAlaLeuAlaGlnSerAsnTh 422
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502 lGlnSerLysThrAspIleIleAsnSerThrAlaLeuProArgProSerValThrThrGl
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R,Walls, D.; Gannon, F. EMBO J. 7, 1191-1196, 1988
A,Title: The expression of novel antigens from the Epstein-Barr virus large internal rep
                                                                                                                A;Accession: S02383
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 88-144 <WAL>
A;Cross-references: BMBL:X07816
C;Genetics: CSTRP 1; BWRF1 2; BWRF1 3; BWRF1 4; BWRF1 5; BWRF1 6; BWRF1 7; BWRF1 8; BWRF1 9;
A;Note: twelve consecutive ORFS apparently encode the identical polypeptide
C;Superfamily: proline-rich protein
C;Keywords: membrane protein; surface antigen
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Tue

R.J.; C.; Ma

RI.

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A;Status: preliminary
A;Molecule type: DNA
A;Residuss: 1.395 <WHI>
A;Residuss: U.395 <WHI>
A;Experimental source: UNIPROT:Q9RVT4; GB:AE001946; GB:AE000513; NID:g6458655; PIDN:AAF1051:
C;Genetics:
                                                                           hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Accession: H75457
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; Mcnonaid, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R A;Reference number: A75250; MUID:20036896; PMID:10567266
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Matches:
Conservative:
Mismatches:
Indels:
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C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Species: Antheraea pernyi (Chinese oak silkmoth)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T3128
R;Sezutsu, H.; Tamura, T.; Yukuhiro, K.
Bubmitted to the EMBL Data Library, August 1998
A;Reference number: 220995
A;Reference number: 220995
A;Accession: T3128
A;Accession: T3128
A;Accession: T3128
A;Accession: T3128
A;Accession: T3128
A;Accession: T3128
A;Cosex-references: UNIPROT:O76786; EMBL:AF083334; NID:g3450882; PID:g3450883; PIDN:AAC3A;Introns: 14/3
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Cispecies: human herpesvirus 2
A;Note: host Homo sapiens (man)
Cispecies: human herpesvirus 2
A;Note: host Homo sapiens (man)
Cipate: 3.1-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
CiAccession: JQ1501
R;McGeoch, D.J.; Cunningham, C.; McIntyre, G.; Dolan, A.
J. Gen. Virol. 72, 3057-3075, 1991
A;Title: Comparative sequence analysis of the long repeat regions and adjoining parts of A;Reference number: JQ1494; MUID:92113549; PMID:1662697
A;Reference number: JQ1501
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-825 <MCG>
A;Cross-references: UNIPROT:P28284; GB:D10471; DDBJ:D01128; NID:g221784; PIDN:BAA23427.1
                                                                                                                                                                                                                                                                                            A;Introns: 25/3; 252/1
C;Superfamily: herpesvirus immediate-early protein IE110; RING finger homology
K;Keywords: DNA binding; immediate-early protein; tandem repeat; transcription regulatio
F;122-127/Domain: RING finger homology <RNG>
F;126-166/Region: zinc finger C3HC4 motif
F;589-623/Region: 5-residue repeats (A-S-S-S-S)
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N;Alternate names: RL2 protein
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                                                                                                                               mucin, tracheal (AMN-22) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession: A37232
R;Gerard, C.; Eddy Jr., R.L.; Shows, T.B.
J. Clin. Invest. 86, 1921-1927, 1990
A;Title: The core polypeptide of cystic fibrosis tracheal mucin contains a tandem repeat A;Reference number: A37232, MUID:91072667; PMID:2254452
A;Reference number: A37232
A;Accession: A37232
A;Accession: A37232
A;Accession: Lyge: mRNA
A;Redouble type: mRNA
A;Residues: 1-294 cGBR>
A;Cross-references: UNIPROT:Q99322; GB:M57417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 ThrProThrProThrGlyThrGlnThrProThrSerThrProlleThrThrThrThrThr
 201
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104
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135
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Mismatches:
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                                525 CACGCCTCCCAGGACCCAGGAGGTTACTCCCTTG
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Matches:
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34.03%
25.65%
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Best Local Similarity:
Query Match:
DB:
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188
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Qy 513 CCCAGGGAATGCCACGCCTCCCAGGAGCTTACTCCCTTGCTGCTGGAGCT 569	Oy 189 ACCACTGCTCCCCAGAACCCACCTGCAGGCACACCAACATGGATGCTGGACTGT 248
- human 22; mucin, MG2a-T1; mucin, MG2a-T2; mucin, 10) 22, 22916; S2914 38brock, A.R.; Levine, M.J. 569, 1993 8equence, and specificity of expression of MUID:9338636; PMID:7690757 (O9UCD8; GB:L13283 andibular gland ffrom NCBI backbone (NCBIN:137719, NCBIP:137 Haraszthy, G.G.; Biesbrock, A.R.; Levine,	Qy 363 TACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCAGATCCTAGGCCTCTGAGGAAGA 422 Db 257 rThrAlaValFroProThrProSerAlaThrThrLeuAspProSerSerAlaBF 277 Qy 423 GGAGGAGCACGACTGCTCCCAGAACCCACGCAGCACACACA
A; Title: Structural features of the low-molecular-mass human salivary mucin. A; Accession: S29115. A; Accession: S29116. A; Molecule type: mRNA A; Residues: 14-168 < RED> A; Accession: S29116 A; Molecule type: protein A; Accession: S29114 A; Molecule type: protein A; Residues: S29114 A; Molecule type: protein A; Residues: S29114 A; Molecule type: protein A; Residues: 143-145, X', 147, XXX', 151-152, X', 154-158, X', 160-161, A', 163-164, XX', 167-1 A; Residues: 143-145, X', 147, XXX', 151-152, X', 154-158, X', 160-161, A', 163-164, XX', 167-1 C; Genetics: A; Gene: GDB: MUC7 A; Cross - references: GDB: 138799; OMIM: 158375 A; Map position: 4q13-4q21 C; Keywords: glycoprotein F; 1-18/Domain: signal sequence #status predicted < SIG>F; 1-18/Domain: signal sequence #status predicted < NAT>F; 97, 128, 135, 146; 312/Binding site: carbohydrate (Asn) (covalent) #status predicted	RESULT 10 T08852 lustrin A - California red abalone Cispecies: Halotis rufescens (California red abalone) Cispecies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 Cispecies: Tolone rufescens r
Alignment Scores: Pred. No.: Pred. No.: Score: Score: Score: Score: J16.00 Marches: Statement Similarity: Best Local Similarity: 10.83\$ Indels: DB: US-10-030-225-1_COPY_58_696 (1-639) x A48018 (1-377)	Alignment Scores: Pred. No.:
45 5 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Qy 618 AGGGTTAGGGGTACTCAAGGTTGGGGGATTCTGGCAGCTT 574

Db 1682AlaGluGluProGlnProAlaLysSerGluAlaAlaProProAlaAsnGlnPr 1699 Qy 196CTCCCCAGAACCCACCAGAGCCACCAACATGGATGCTGGAC 245 1699 OPheSerArgPheGlnValThrProIleGlnAlaSerProValLeuHis	1764 olenArgGinProThrAlaThrPheValPheThrGiuArgGiuGlyGluProileProVa 447 AACCCACTGCAGGCAGAGCTACCCACATGGATGTTGGACTGTCACTGAGCCAGCGCGCGC	Db 1803 aProValProSerSerSerMetProSerAlaSerGluAlaMetProArgSerAlaGlyTr 1823 Qy : 532CCCAGGACCCAGGAGGTTACTCCCTTGCTGGAGCTGCAGAAGCTGCCAGAATT 587	RESULT 12 QORBE BPLEI PORTEI C;Species: human herpesvirus 4 (strain B85-8) C;Species: human herpesvirus 4, Epstein-Barr virus C;Species: human herpesvirus 4, Epstein-Barr virus C;Date: 25-Feb-1985 #sequence revision 25-Feb-1985 #text_change 09-Jul-2004 C;Accession: G93065; A03747; S32.93 R;Bankier, A.T.; Deininger, P.L.; Parrell, P.J.; Barrell, B.G. Mol. Biol. Med. 1, 21-45, 1983 A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus A;Reference number: A93065; MUID:85035713; PMID:6092825 A;Accession: G93065 A;Accession: G93065 A;Residues: 1-3149 <aba> A;Residues: 1-3149 <aba> A;Cross-references: UNIPROT:P03186; EMBL:V01555; NID:G59074; PIDN:CAA24839.1; PID:G13348</aba></aba>	R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H Nature 310, 207-211, 1984 A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome. A;Reference number: A03794; MUID:84270667; PMID:6087149 A;Contents: annotation; protein coding region C;Superfamily: human herpesvirus 4 BPLF1 protein Alignment Scores: Pred. No.: 125.00 Matches: 65 percent Similarity: 39.57% Conservative: 28	Best Local Similarity: 27.66% Mismatches: 85
Qy 453 GTGGGTTCTGGGGAGCAGTCGTCCTCCTCCTCCTCCTCAGAGGCCTAGGATCTGGGGA 394 Db 1024SerGlySerGlySerGerSerGlySerSerSerGlySerSerSerGlySerGlySerGlySerSerSerGlySerSerGlySerGlySerGlySerGlySerSerSerGlySerSerSerGlySerSerSerGlySerSerGlySerSerGlySerSerGlySerSerGlySerSerGlySerSerGlySerSerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerGlySerSerGly	168 AGGCTCGAGGAGGCTGAGACCTCTGCGAGGCTCGTGAGGCTCCCAGGCGTGG 1100 fdlySerdlySerGlySerSerSerSerGlySerTGlySerGl 108 TCGGGGAGC	Qy 63 CAGCAGCGCAGCAGCAGC 42 b 1135 ySerGlySerGlySerSerSer 1142 RESULT 11 T51023 T51023 hypothetical protein B7F21.40 [imported] - Neurospora crassa C;Species: Neurospora crassa C;Date: 21-301-2000 #sequence revision 21-301-2000 #text change 09-Jul-2004	; Holland, R.; Nyakatura,	0.103 Length: 2649 126.00 Matches: 56 25.34% Mismatches: 81 10.83% Indels: 61 2 Gaps: 8	Oy 24 CGGCTCCTCTGCGTGCTGCTGGGGGGCTGCTGGAGGCGCTAGGGCTCCC 83

532 GTCACCTGGTTATCAGGGTTAGGGGTACTCAAGGTTGCGTGGACCAATTCTGGCAGCTTC 573

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Qy 72 GCTAGGGCTCCCCGTGAAGAAGCCGCGGGCTCCGCGGACCACGGCCTGGGAGCCTCAC 128		DD 409 ProGinThrProLysArgLysLysGlyLeuGlyLysAspSerProHisLys 425	Qy 129 GAGGCTCGCAGAGGTCTCAGCCTCCCAGATCCTAGGCCTCTGAAGGAAG	ProThrSerdlyArgArgLeuProLeuSerSerThrThrAsp-ThrGluAspA	QY 189 ACCACTGCTCCCCAGAACCCACTGCAGGCAGAG		TGAGCCAGCA	Db 463 oProProVallleProlleProHisGlnSerProProAlase 477	Qy 264 CATGACCCCAGGCAACACCCCTCCCAGGACCCCAGAGGTTACTCCGTTG 315		Oy 316 -CGGCTGGAGCTCCAGAAGCTGCCGGGATTGGCCAGCACACC 357	Db 496 oArgLeuProLeuGlnIleProIleProLeuProGlnAlaAlaProSerAsnProLysIl 516	Qy 35817GAGTACCCCTGATACCCAGGCTTCGGCTCCCCA 399	Db 516 eProLeuThrThrProSerProSerProThrAlaAlaAlaAlaProThrThrThrThrLe 536	OY 400 -GATCCTAGGCCTCTGAGGGAAGAGGAGGACGACTGCTCCCCAGAACCCACCTGCA 458	Db 536 uSerProProThrGlnGlnGlnProProGlnSerAlaAlaProSerProLe 556	Qy 459 GGCAGAGCTACACCAACATGGATGTTGGACTGTCACTGAGCCAGGCAGCCCTGACGG 518	Db 556 uLeuProGlnGlnBroThrProSerAlaAlaProAlaProSerProLeuLeuProGl 576	OY 519 GAATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGCAGAGCTGCAGAA 575	Db 576 nGlnGlnProProSerAlaAlaArgAlaProSerProLeuProProGlnGlnGlnPr 596	Qy 576 GCTGCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT 618	Db 596 oLeuProSerAlaThrProAlaPro 604	RESULT 13 .	19332) WSC4 homolog [imported] - yeast (Kluyveromyces marxianus var. lactis) C:Sheries: Kluvveromyces marxianus var. lactis. Candida enhaerica	CiDate: 1.11/2.2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004	C,ACCEBION: 173223 R,BBO, W.G.; Fukubara, H. submitted to the FMBara, July 1999	A. Description: The ubiquitin-encoding genes of Kluyveromyces lactis. A. Reference number: 223000	A;Accession: T45525 A;Status: preliminary; translated from GB/EMBL/DDBJ A:Majoria trans. Dans	A; NOICCULE 179: DAA A; Residues: 1-446 <bao> A; Cross-references: UNIPROT: Q9Y849; EMBL: AJ243800; PIDN: CAB50897.1 A: Experimental source: strain 2359/152</bao>	C;Genetics: A;Gene: wsc4	0.179 Length: 123.50 Matches:	Best Local Similarity: 26.03% Mismatches: 92 Query Match: 10.55% Indels: 57 DB: 2 Gaps: 9

US-10-030-225-1_COPY_58_696 (1-639) x T45525 (1-446)

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thyl-D-aspartate receptor chain NMDAR2D-2 - rat ecies: Rattus norvegicus (Norway rat)
te: O2-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
te: O2-Aug-1996 #sequence revision 02-Aug-1996 #text_change 09-Jul-2004
te: D3-178557 IS8158; D45219
nyer, H.; Burnashev, N.; Laurie, D.J.; Sakmann, B.; Seeburg, P.H.
on 12, 529-540, 1994
tle: Developmental and regional expression in the rat brain and functional propertie ference number: IS8158; MUID:94206533; PMID:7512349
cession: I78557
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lecule type: mRNA
sidues: 1-1323 GRES>
oss-references: UNIPROT:Q62645; GB:L31612; NID:g469068; PIDN:AAC37647.1; PID:g469069
cossion: 158158
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A;Molecule type: mRWA
A;Molecule type: mRWA
A;Residues: 1-66, 'V', 68-1323 <RE2>
A;Cross-references: GB:LJ1611; NID:9469066; PIDN:AAC37646.1; PID:9469067
B;Ishii, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, M.; Akazawa
                                                                                                   ---AGCAGCAAGGAGTA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 TCCTCCTCTTCCCTCAGAGGCCTA-----GGATCTGGGGAGGCTGAAGCCTGGGTATCA 375
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                                                                                                                                                                                                                                                                                                                                                                                        488 GTCCAACATCCATGTTGGTGTAGCTCTGCCTGCAGGTGGGTTCTGGGGAGCAGTCGTGGTGCC 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 SerAladlyLeuTyrGlyTyrLeuTyrLeuGlySerGlySerLeuProSerIleSerSer 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 ACAGTCCAGCATCCATGTTGGTGTGGCTCTGCCTGCAGGTGGGTTCTGGGGAGCAGTGGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 ThrSerAsp-----SerSerSerAlaThr-----SerSerSer 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 GCCTCCTCCTCTTCCTTCAGAGGCCTAGGATCTGGGGAGGCTGAGACCTCTGCGAGCCTC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerSerSerThrSerSerThrSerSerSerSerSerSerSerSerSerSerSer 198
                                                                                                                                            ||| ::: :: 75 SerValSerSerCysSerGluThrCysProGlyYrglyValGluAspCysGlyAspThr 94
128 GTGAGGCTCCCAGGCCGTGGTCCGCGGAGCCGCGGCTTCTTCACGGGGAGCCCTAGCGCC 69
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44 CysSerAspThrCysArgGlyLysSerPheAspPheAlalleValGlnGly-----
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M.; Akazawa

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                                                                                                                 CjAccession: C45219
R;Ishli, T.; Moriyoshi, K.; Sugihara, H.; Sakurada, K.; Kadotani, H.; Yokoi, J. Biol. Chem. 268, 2816-2843, 1993
A;Title: Molecular characterization of the family of the N-methyl-D-aspartate A;Reference number: A45219; MuID:93155102; PMID:8428958
A;Accession: C45219
                                                                                                                                                                                                                                                                                                                               receptor homology
                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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J. Biol. Chem. 268, 2836-2843, 1993
A;Title: Molecular characterization of the family of the N-methy
A;Reference number: A45219; MUID:93155102; PMID:8428958
A;Accession: D45219
A;Actus: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1265-1333 «ISH»
A;Exporimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIP:124265)
C;Superfamily: N-methyl-D-aspartate receptor 2D; glutamate recep
F;451-879/Domain: glutamate receptor homology «GRH»
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Search completed: February 19, 2005, 00:23:05 Job time : 51 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaf29348 Human pro Aaf93820 Human cDN Aaf94019 Primer sp		Probe	Aba21690 Probe #15	Aak25606 Human bon	Human	Abs25182 Human liv	Aai00170 Probe #16	Abs00175 Human gen	Aai19514 Probe #94	Aba64531 Human foe	Aai44705 Probe #13	Aba46659 Human bre	Aba31664 Probe #10	Aak38709 Human bon	Aak12982 Human bra	Abs38283 Human liv
IES	Dead	Aaf2 Aaf9 Aaf9	Aail	Aai3	Aba2	Aak2	Aak0	Abs2	Aaio	Abso	Aail	Aba6	Aai4	Aba4	Aba3	Aak3	Aakl	Abs3
SUMMARIES	ΩI	AAF29348 AAF93820 AAF94019	AAI10232	AAI31480	ABA21690	AAK25606	AAK00167	ABS25182	AAI00170	ABS00175	AAI19514	ABA64531	AA144705	ABA46659	ABA31664	AAK38709	AAK12982	ABS38283
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Aai05236 Probe #52 Abs12780 Human gen Adf58409 Human pol Abo30568 Oligonucl	Abq30569 Oligonucl Abq30566 Oligonucl Abq30567 Oligonucl Abq10430 Pseudomon Abq10367 Pseudomon	Abd10513 Pseudomon Add64839 Novel hum Aah78274 Coding se Aah78273 Nucleotid		Adr08320 Fuil leng Aar68715 Streptomy Aca61566 Streptomy Aca61565 Streptomy Aal44951 Equine he	מלחדוום
AAI05236 ABS12780 ADF58409 ABO30568	ABQ30569 ABQ30566 ABQ30567 ABD10430	ABD10513 ADQ64839 AAH78274 AAH78273	AAS27841 AAS35091 AAK80295 AAB94644 ·	ADR08320 AAT68715 ACA61566 ACA61565 AAL444951	ADE/4611
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ALIGNMENTS

This invention relates to polynucleotide sequence PSEC137, which encodes a human proliferation differentiation factor protein. Included in the invention is a vector containing the CDNA sequence, a transformant containing the vector, and a process for producing the protein. The protein together with its encoded DNA and antisense DNA are used in drugs to maintain the haematopoietic function. The present sequence represents obNA encoding the proliferation differentiation factor protein Human; proliferation differentiation factor; haematopoietic function; ss. Proliferation-differentiation factor protein encoded by PSEC137 cloned from human cDNA library, being hematopoietic factor for inducing differentiation of blood cells, used to maintain hematopoietic function. Yoshida K, Masuho Human proliferation differentiation factor cDNA sequence. Kawai Y, Claim 1; Page 36-41; 49pp; Japanese. BP. Isogai T, Nishikawa T, AAF29348 standard; cDNA; 2981 06-JUL-2000; 2000WO-JP004514. 99JP-00194179. (first entry) (HELI-) HELIX RES INST. WPI; 2001-138354/14. P-PSDB; AAB49765 WO200104312-A1. 08-JUL-1999; 18-OCT-1999; Homo sapiens 18-JAN-2001. 20-APR-2001 AAF29348; Ota T, AAF29348 RESULT 1 CCCCCCCXXX444X88X54X4X6XXXXXXXXXXXXXXXXXXXX

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                                                     Length 2981;
                Sequence 2981 BP; 609 A; 925 C; 887 G; 560 T; 0 U; 0 Other;
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                                                Ouery Match
100.0%; Score 639; DB 4;
Best Local Similarity 100.0%; Pred. No. 4e-142;
Matches 639; Conservative 0; Mismatches 0;
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rheumatoid arthritis; diabetes; ss.
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which encode human secretory or membrane proteins represented by AAB88317

"AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polymucleotide sequences can be used in gene
c therapy. The polymucleotide sequences and the proteins they encode may be
therapy. The polymucleotide sequences and the proteins they encode may be
c therapy. The polymucleotide sequences and the protein expression. The
c used in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
c nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
c and quantitate the presence of similar nucleic acid sequences in samples.
CT They may also be used to study the expression and function of secretory
proteins/membrane polypeptides and their role in metabolism. The
colypeptides may be used as antigens in the production of antibodies
c against them and in assays to identify modulators (agonists and
activity. The antibodies may also be used as diagnostic agents for
c activity. The antibodies may also be used as diagnostic agents for
c detecting the presence of the polypeptides in samples (e.g. by enzyme
collinked immunosorbant assay (ELISA). Examples of diseases which may be
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control of the polypeptides in samples (e.g. by enzyme
control of the polypeptides in samples (e.g. by enzyme
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                                                                                                                                                                                                                                                                    Hayashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding secretory proteins/membrane proteins, usefi
gene therapy or as candidate target molecules in drug development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 153; 609pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                    Sugiyama T,
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treated include rheumatoid arthritis and diabetes
                                                                                                                                                                                                                                                               Kawai Y,
                                                                                                                                                                                                                                                      Ota T, Isogai T, Nishikawa T,
08-JUL-1999; 99JP-00194179.
11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
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Matches 639; Conservative (
                                                                                                                                                                          (HELI-) HELIX RES INST.
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AAB88419. Included in the invention are primers AAF9317 - AAF94295 and
AAF62323 - AAF62235 which are used to isolate the cDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polynucleotide sequences can be used in gene
therapy. The polynucleotide sequences and the proteins they encode may be
used in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and quantitate the presence of similar nucleic acid sequences in samples. They may also be used to study the expression and function of secretory proteins/membrane polypeptides and their role in metabolism. The polypeptides may be used as antigens in the production of antibodies against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and
                                                                                                                                                                                                                                                                                                                                453.
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                                                                                                           CAGGAGGTTACTCCCTTGCTGGAGCTGCAGAAGCTGCCAGAATTGGTCCACCAACC
                                                                                                                          CAGGAGGTTACTCCCTTGCTGCTGGAGCTGCAGAAGCTGCCAGAATTGGTCCACGCAACC
           TGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGAATGCCACGCCTCCCAGGACC
                                                                                  TGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCCACGCCTCCCAGGACC
                                                                                                                                                                                                                                                                                                                              Primer specific for DNA encoding secretory/membrane protein SEQ ID
                                                                                                                                                                                                                                                                                                                                                       Human; secretory protein; membrane protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy or as candidate target molecules in drug development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins/membrane proteins,
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                                                                                                                                                                            TTGAGTACCCCTAACCCTGATAACCAGGTGACCATCAAG 696
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
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                                                                                                                                                                                                                                                   AAF94019 standard; DNA; 750
                                                                                                                                                                                                                                                                                                     (first entry)
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may be
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                                                                                                                                                                                                                                                                          CTGGAGGCGGCGTAGGGCTCCCCGTGAAGAAGCCGCGGGCTCCGCGGCCACCACGGCCTGGG
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                 detecting the presence of the polypeptides in samples (e.g. by linked immunosorbant assay (ELISA). Examples of diseases which treated include rheumatoid arthritis and diabetes
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activity. The antibodies may also be used as diagnostic agents
                                                                                                                             Length 750;
                                                                                       Sequence 750 BP; 170 A; 249 C; 215 G; 109 T; 0 U; 7 Other;
                                                                                                                                                             Indels
                                                                                                                         84.9%; Score 542.6; DB 5;
96.9%; Pred. No. 2.5e-119;
iive 0; Mismatches 12;
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Matches 616; Conserv
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CCAGGAGGTTACTCCCT
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                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                           The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. Notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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1.4e-52;
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77.3%; Pred. No. 1.4e
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 165; 487pp; English
                                                                                                                                                                                          Rank DR;
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                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                          Chen W,
                                                      2000US-0180312P.
2000US-0207456P.
2000US-00608408.
                                                                                               2000US-00632366
                                                                                                          2000US-0234687P
2000US-0236359P
                                                                                                                                       04-OCT-2000; 2000GB-00024263
                              2001WO-US000670
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                                                                                                                                                                                                                    WPI; 2001-488901/53
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                                                                                               03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                              30-JAN-2001;
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foctal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
                                                                                                                                                    Human foetal liver single exon nucleic acid probe #173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 261.8; DB 4;
Pred. No. 1.4e-52;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at ftp.wipo.int/pub/published_pct_sequences
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                DNA; 497 BP
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2000US-00608408.
2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                          (first entry)
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.868/c
ABA51868 standard;
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30-JUN-2000; 2
03-AUG-2000; 2
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ACATGGATGCTGGACTGTCACTGACTGACCGGCGAGCCATGACCCCCAGGCAACGCCACCCCTCC
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                      CAGGACCCCAGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAG
                                                                                                                                                                                                                  TCCTGGCTCTGCCTGGCCTGTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCAC
                                              ACATGGATGCTGGACTGTCACTGAGCCAGCCATGACCCCAGGCAACACCACCCTCC
                                                                                                                                                                                                                                         ----CAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGA
                                                                                                                                                                                                                                                              CTCACCTTCCCTCTCTCTCTCAGGCTTCAGGCTCCCCCAGATCCTAGGCCTCTGAGGGA
                                                                                                                                                                                                                                                                                         Probe #156 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
                                                                                                                                            CACAACCTTGAGTACCCCTAACCCTGATACC-----
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2000US-0234687P.
2000US-0236359P.
2000GB-00024263.
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21-SEP-2000;
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04-OCT-2000;
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                                                                     197 CTCACCTTCCCTCTCTTCCTCAGGCTTCAGCCTCCCAGATCCTAGGCCTCTGAGGGA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                        AGAGGAGGCACGCACCGCCCAGAACCCACCTGCAGGAGCCAACACCAACATGG 78
                                                                                                                                                         ATGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCAGGAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                      257 TCCTGGCTCTGCCTGGCCAGCCTTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCAC
                                                                                           ATGTTGGACTGTCACTGAGCCAGCCCTGACCCCCAGGGAATGCCACGCCTCCCAGGAC
                                                                                                                                                                                                                                                                                                                                                   to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.0%; Score 261.8; DB 4; Length 497;
Best Local Similarity 77.3%; Pred. No. 1.4e-52;
Matches 384; Conservative 0; Mismatches 2; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                           Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 25; SEQ ID NO 166; 654pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
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30-JUN-2000; 2000US-0060B40B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-02346B7P.
27-SEP-2000; 2000US-023459P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                          CCAGGAGGTTACTCCCT 556
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                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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382
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WPI; 2001-488899/53

Gaps

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, sraging, sraging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                     438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 CTCACCTTCCCTCTCTTCCTCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGG 138
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                   gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                  2; Indels 111;
                                                                                                                                                                                                                                                                                                                              41.0%; Score 261.8; DB 4; Length 497; 77.3%; Pred. No. 1.4e-52; Indels 111; ive 0; Mismatches 2; Indels 111;
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                                                                                                                                                                                                                                                                                                Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
                 exon nucleic acid probes for analyzing
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                                                               Claim 1; SEQ ID NO 156; 530pp; English.
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ID AAK25606 standard; DNA; 497
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Matches 384; Conservative
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Best Local Similarity
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                                                                 Example 4; SEQ ID NO 163; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                  Rank DR
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                                                                                                                                     26-MAY-2000; 2000US-0207456P.
30-UUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234589P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                  Chen W,
                                                                                               30-JAN-2001; 2001WO-US000668
                                                                                                                         2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                               the probes of the invention
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les 384; Conserv
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                                       WO200157276-A2
              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis,
                                                                                                                                                                                                                                                                                          CACAACCTTGAGTACCCCTAACCCTGATACCCAGGTGAGAGCTACAGAAGGGCCAGCAGC
                                                                                      257 ICCTGGCTCTGCCTGGCCAGCCTTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCAC
                                                                                                                                                                                               197 CTCACCTTCCCTCTCTTCTTCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, single exon nucleic acid probe, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia, hyperlipidaemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human liver single exon probe, SEQ ID No 172.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 172; 658pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                           556
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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ID ABS25182 standard; DNA; 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple scherosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGACCCCAGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAG 350
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                                                                                                                                                                                                                                                                  Human; brain expressed exon; gene expression analysis; probe; microarray;
Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGGACCCCAGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.0%; Score 261.8; DB 4; Length 497; 77.3%; Pred. No. 1.4e-52; ive 0; Mismatches 2; Indels 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 158; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                               Human brain expressed single exon probe SEQ ID NO: 158.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                      AAK00167 standard; DNA; 497
                CCAGGAGGTTACTCCCT
CCAGGAGGTTACTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCCAGGAC 18
                                                                                                                                                                                                                                                                                                                                                                                                                         CTCACCTTCCCTCTCTCTCTCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGA
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                                                                                                                                                                                                                                                                                                                                                                                               CAGGACCCCAGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 TCCTGGCTCTGCCTGGCCAGCCTTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCAC
                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                            111;
                                                                                                                                                                 Query Match 41.0%; Score 261.8; DB 4; Length 497; Best Local Similarity 77.3%; Pred. No. 1.4e-52; Matches 384; Conservative 0; Mismatches 2; Indels 111.
                                                                                                                                 Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGAGGTTACTCCCT 556
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AAI00170/
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2000US-0180312P. 2000US-0207456P.

04-FEB-2000; 26-MAY-2000;

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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, breast. The probes are useful for predicting, diagnosing, grading, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and noncarcinoma tumours. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                         gene expression in
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                                                                                                                                                                                                                                                                                                                                         measuring
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                                                                                                                                                                                                                                                                                                                                Novel single exon nucleic acid probe used
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 161; 322pp; English
                                                                                                                                                                                                                            Rank DR
                                                                                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
                                                                                                            04-OCT-2000; 2000GB-00024263
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The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from thuman lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryotic genome, comprising (a) adjorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single exon comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon comprising one expression of the exons in the tissues and/or cell types using hybridisation or encoded by the cycobes/open reading frames (ORF). The probes are used for gene expression analysis, and for identifying exons in a gene, particularly using human analysis, and for identifying exons in a gene, particularly using human
                                                                                                                                                                                                                                                                                          Hermansky-Pudiak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                              Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
bronic obstructive pulmonary disease; interstitial lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                        probe from lung SEQ ID No 166
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                                                                                                                                                                        Human genome-derived single exon
                                          ABS00175 standard; DNA; 497 BP
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2000US-0234687P.
2000US-0236359P.
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                                                                                                                             (first entry)
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21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                             19-AUG-2002
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RESULT 12
ABS00175/c
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 derived mRNA and for the study of lung diseases such as asthma, lung
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             cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 ATGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCAGGAC 18
                                                       Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                  Indels 111;
                                                                                                                                                                                                                                   Length 497;
                                                                                                                                                                                                     Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 DB 6;
                                                                                                                                                                                                                                   Score 261.8; DB 6;
Pred. No. 1.4e-52;
0; Mismatches 2;
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                                                                                                                                                                                                                                                  Similarity
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Best Local Simil
Matches 384; C
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40200157278-A2

Penn SG,

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Shote: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #13391 used to measure gene expression in human placenta sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.5%; Score 239.8; DB 4; Length 243; 99.2%; Pred. No. 2.1e-47; ative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; SEQ ID NO 12836; 639pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                       Chen W, Rank DR
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                             30-JAN-2001; 2001WO-US000669
                                                                                                                                                                       2000US-0180312P
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                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                              WO200157277-A2
      Homo sapiens.
                                                                                                                                                                                           26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGCTGCAGAAGCTGCCGGGATTGGCCACACCTTGAGTACCCCTAAACCTGATACC 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human foetal liver single exon nucleic acid probe #12836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 9447; 487pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                 Chen W, Rank DR
                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                               04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
                                                                                                                                             03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
                                       30-JAN-2001; 2001WO-US000670
                                                                                                                                                                                                             04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 AGAACCCACCTGCAGGCAGAGCCACACATGGATGCTGGACTGTCACTGAGCCAGCA 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 243 BP; 34 A; 61 C; 89 G; 59 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 25; SEQ ID NO 13391; 654pp; English
                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK, Chen W, Rank DR,
                                                                                                                                                                                                                                                                                            (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                 30-JUN-2000; 2000US-00608408.
03-MG-2000; 2000US-00532366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02353595.
04-OCT-2000; 2000GB-00024263.
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26-MAY-2000; 2000US-0207456P.
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Matches 241; Conservative
                 genetic disorder; ss
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Sequence 9, Appli
Sequence 8860, Ap
Sequence 3298, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
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16965, A
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Sequence 8971, Ap
Sequence 9117, Ap
                                                                               22:06:55; Search time 158 Seconds (without alignments) 6617.600 Million cell updates/sec
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Sequence 2,
Sequence 169
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5: /egn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /egn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5.1.6
Compugen Ltd
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US-09-252-991A-8971
US-09-252-991A-8117
US-09-902-540-6461
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US-09-823-938A-9
US-09-252-991A-8860
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US-09-105-537-1
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US-09-091-609-1
US-08-091-609-1
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US-08-091-609-3
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US-10-237-551-119
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US-10-237-551-214
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US-09-252-991A-6159
US-09-252-991A-6012
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GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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| Gapop 10.0 , Gapext 1.0
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Pagence 9334, Application US/09252991A

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Pagence 9334, Application US/09252991A

Pagence 9334, Application US/09252991A

APPLICAMT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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; Patent No. 6551795
; GENERAL INFORMATION: APPLICATION APPLICANT: MATE J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
Sequence 1, Appli
Sequence 7346, Ap
Sequence 8236, Ap
Sequence 851, App
Sequence 1057, Ap
Sequence 16924, A
Sequence 16924, A
Sequence 1698, A
Sequence 17202, A
Sequence 6461, Ap
Sequence 483, App
Sequence 483, App
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Sequence 4214, Al
Sequence 1424, Al
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Pred. No. 0.1;
); Mismatches 112; Indels
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US-09-949-016-12364
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; ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity
Matches 112; Conserv
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316 CGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTGAGTACC--CCTAACC 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 GCAGAGGICTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGCACCACTG
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                                                                                                                                                                                                                                                                               APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: State, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: Wiegand, Noger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses 'S PILE REPERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 2001-07-10
PRIOR PILING DATE: 2001-07-10
NUMBER OF SED ID NOS: 16825
SEQ ID NOS: 16825
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                                                              699 GCTGACGTAGGCGCCCTCCTTCGCCACGCGCAGCAACGGCA 656
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Pred. No. 0.22;
0; Mismatches 244; Indels
                           187 GCACCACTGCTCCCCAGAACCCACCTGCAGGCCAGAGCCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)..(1494)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-6461
                                                                                                                                                                                                      ; Sequence 6461, Application US/09902540; Patent No. 6833447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 452, Application US/09902540; Patent No. 6833447
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Best Local Similarity 46.3%;
Matches 215; Conservative
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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US-09-902-540-452/c
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 9117
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                           Length 1464;
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                                                                                                                                                                                                                                                                                                                                                                                           7.0%; Score 44.8; DB 4; 50.0%; Pred. No. 0.11;
                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR FILING DATE: 1998-02-18
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
SEQ ID NO 8971
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; Sequence 9117, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Matches 112, Conservative
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Best Local Similarity
Matches 112; Conserv
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TYPE: DNA ORGANISM: Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR PLILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 452
LENGTH: 1664
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1664;
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Pred. No. 0.23;
0; Mismatches 244; Indels
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Patent No. 6242419
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Abernethy, Nevin
APPLICANT: Gurust, Rene
APPLICANT: Munison, Greg
TITLE OF INVENTION: Compounds isolated from stroy
TITLE OF INVENTION: Compounds isolated from stroy
TITLE OF INVENTION: and methods for their use
FILE REFERENCE: 11000.1037c1
                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(1664)
; OTHER INFORMATION: unsure at all n locations US-09-902-540-452
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                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Myxococcus xanthus
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Best Local Similarity
Matches 215; Conserva
                                                                                                                                                                                                                                                                                                                        NAME/KEY: unsure
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Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Sleeman, Matthew
APPLICANT: Aleeman, Matthew
APPLICANT: Abenethy, Nevin
APPLICANT: Mumble, Anand
APPLICANT: Cumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1037c3
CURRENT APPLICATION NUMBER: US/09/823,038A
CURRENT FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                  Length 815;
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                                                                                                                                                                                                                                                                                                           Score 42.2; DB 3;
Pred. No. 0.43;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.2; DB
Pred. No. 0.43;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/383,586
CURRENT FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 38
SEQ TWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09823038A Patent No. 6797271 GENERAL INFORMATION:
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Best Local Similarity 70.9%;
Matches 56; Conservative
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NAME/KEY: sig peptide
LOCATION: (119)...(205)
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Best Local Similarity
Matches 56; Conserv
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                                                                                                                       TYPE: DNA
ORGANISM: Mouse
FEATURE:
NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 GCTGCTGCTGGCGCCGCTGGAGGCGCGCTAGGGCTCCCCGTGAAGAAGCCGCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 3; Length 15872;
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APPLICANT: SHERMAN, DAVID H.
APPLICANT: WILLIAMS, MARK D.
APPLICANT: WILLIAMS, MARK D.
TITLE OF INVENTION: METABOLIC ENGINEERING OF
TITLE OF INVENTION: DOLYHUTORXYALKANOATE MONOMER SYNTHASES
FILE REFERENCE: 600.297US2
CURRENT APPLICATION NUMBER: US/09/091,609
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: PCT/US96/20119
EARLIER FILING DATE: 1998-12-18
EARLIER FILING DATE: 1995-12-19
WUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sherman, D.H.
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin FILER REFERENCE: 600-438USI
CURRENT APPLICANTON NUMBER: US/09/105,537A
CURRENT PFILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 46.0%; Pred. No. 3.6;
Matches 134; Conservative 0; Mismatches 157; Indels
                                                                                    974 gcaccecracceaccaccragaderes
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190 CCACTGCTCCCCAGAACCCACCTGCAGGC
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09105537A Patent No. 6265202
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Patent No. 6600029
GENERAL INFORMATION:

j ORGANISM: Streptomyces venezuelae
US-09-105-537-1
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3298
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Pred. No. 0.73;
0; Mismatches 88; Indels
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                        CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
LENGTH: 732
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ORGANISM: Pseudomonas aeruginosa
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il Similarity 51.6%;
94; Conservative
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Matches 104; Conservative
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US-09-252-991A-3298
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US-09-252-991A-3298
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Best Local
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  8893 CCGGCTGGTGCCCGAGGGCTCGGAGGCTATCTGCTGACCGGCAGCGCCGACGCGGTGAT 8952
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                                               GCCACACCAACATGGATGCTGGACTGTCACTGAGCCAGCAGCCATGACCCCAGGCAACAC
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Pred. No. 4.7;
0; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DeHoff, Bradley S.
APPLICANT: Mibtores, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUMPATIBATION COMPACTOR
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCI(DOS) Text only
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C
FILLING DATE: February 21, 1997
CLASSIFICATION: 435
ATTORNEY, AGENT INFORMATION:
NAME: Plant, Thomas, G.
REGISTRATION NUMBER: 35,784
REGISTRATION NUMBER: 35,784
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/08804227C; Patent No. 5876991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: LILLY CORPORATE CENTER
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IBM Compatible
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 46.05
Matches 134; Conservative
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31232..36067
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MEDIUM TYPE: Floppy
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LOCATION:
FEATURE:
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US-08-804-227C-1
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US-08-804-227C-1
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                                                                                                                                    DB 4; Length 15872;
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APPLICANT: SHERMAN, DAVID H.
APPLICANT: SHERMAN, DAVID H.
APPLICANT: WILLIAMS, MARK D.
APPLICANT: WILLIAMS, MARK D.
APPLICANT: WILLIAMS, MARK D.
TITLE OF INVENTION: POLYHYDROXYALKANOATE MONOMER SYNTHASES
FILE REPERENCE: 600.297US2
CURRENT APPLICATION NUMBER: US/09/091,609
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: PCT/US96/20119
EARLIER FILING DATE: 1996-12-18
EARLIER FILING DATE: 1995-12-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                0; Mismatches 157; Indels
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                                                                                                                                    Score 39.8; DE
Pred. No. 3.6;
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Pred. No. 3.
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ORGANISM: Streptomyces venezuelae
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Patent No. 6600029
                                                                                                                                 6.2%;
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; LOCATION: (14148)...(15824)
US-09-091-609-3
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Best Local Similarity 46.0
Matches 134; Conservative
                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(13909)
US-09-091-609-1
                                                                                                                                                         Best Local Similarity
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                                                                                                                                                                              Matches 134;
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                                                                                                                                    Query Match
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CURRENT FILING DATE:
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
36635 GCTGCTGGAGGTGTCCTGGGAGGCGCTGGAACGCGCGGGGATCGACCGTCCTCGCT
                                                                                                                                                                                                                                                                                                                       CCGCGCGACCACGGCCTGGGGAGCCTCACGAGGCTCGCAGAGGTCTCAGCCTCCCCAGATCC
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: PRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBRECULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Patent No. 6294328
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Matches 85; Conservative
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GENERAL INFORMATION:
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US-09-949-016-16965
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US-09-103-840A-2/c
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Sequence 16965, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 16965
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Job time : 166 secs
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51.8%;
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Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
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February 21, 2005, 23:10:41; Search time 500 Seconds (without alignments) 7553.614 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB_seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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639
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 156, App	Sequence 16984, A	Sequence 17159, A	Sequence 17160, A	Sequence 17157, A	Sequence 17158, A	Sequence 25086, A	Sequence 165209,	Sequence 6, Appli	Sequence 4, Appli	Sequence 1501, Ap
	01	US-09-864-761-156	US-09-864-761-16984	US-10-363-345A-17159	US-10-363-345A-17160	US-10-363-345A-17157	US-10-363-345A-17158	US-10-425-114-25086	US-10-425-115-165209	US-09-802-127-6	US-09-802-127-4	US-09-764-868-1501
	DB	6	σ	18	18	18	18	17	18	σ	σ	6
	Query Match Length DB ID	497	243	1128	1128	1128	1128	1770	1770	3018	3391	5968
%	Query Match	41.0	37.5	14.4	14.4	13.4	13.4	7.2	7.2	6.7	6.7	6.7
	Score	261.8	239.8	91.8	91.8	85.6	85.6	46.2	46.2	42.6	42.6	42.6
	Result No.	C 1	7 0	m	Ω 4	c 2	9	7	80	6	10	11

Sequence 619, App Sequence 13512, A	Sequence 9, Appii Sequence 163054,	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Ä	999									Sequence 991, App	Sequence 117, App	Sequence 94260, A	Sequence 66678, A	Sequence 22196, A	Sequence 94549, A	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli				-		٠.		Sequence 132758,
14 US-10-103-313-619 18 US-10-437-963-13512	9 US-U9-823-U38A-9 18 US-10-425-115-163054	18 US-10-626-832-1					18 US-10-425-115-88722			18 US-10-322-281-782	18 US-10-672-764A-31	18 US-10-437-963-25745				11 US-09-764-875-117		18 US-10-437-963-66678		18 US-10-425-115-94549	US-09-861-289-1	9 US-09-860-846-1			16 US-10-271-889-44			13 US-10-027-632-132758	13 US-10-027-632-132759	13 US-10-027-632-132760	17 US-10-027-632-132758
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ALIGNMENTS

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APPLICANT: Rank, David R.
APPLICANT: Haracal, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PILING DATE: 2000-03-04
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/USO1/00669
APPLICATION NUMBER: PCT/USO1/00665
FILING DATE: 2001-01-30
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Sequence 156, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        437 ACATGGATGCTGGACTGTCACTGAGCCAGCAGCCATGACCCCAGGGAACGCCACCCTCC
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N: EXPRESED IN BY474, SIGNAL = 0.85
N: EXPRESSED IN BY474, SIGNAL = 0.92
N: EXPRESSED IN HELLOO, SIGNAL = 0.92
N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75
N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.92
N: EXPRESSED IN ADULT LIVER, SIGNAL = 0.96
N: EXPRESSED IN BEAN, SIGNAL = 1
N: EXPRESSED IN HELA, SIGNAL = 1
N: EXPRESSED IN HELA, SIGNAL = 1.4
                                 PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SEQ ID NO 15: 497
PRIOR PILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
PRIOR PILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
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NUMBER: OF DE DIOR SEQUENCE Listing Engine vers: 1.1
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           APPLICATION NUMBER: PCT/US01/00668
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Matches 384; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: MACCHER INFORMATION: ED OTHER INFORMATION: ED O
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| TITLE OF INVENTION: GIBBE WEREASION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: GIBBE WEREASION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: GIBBE WEREASION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: GIBBE WEREASION ANALYSIS BY MICROARRAY
| TITLE OF INVENTION: GIBBE WEREASION ANALYSIS BY MICROARRAY
| TITLE OF THE REPORT OF WINDSER: US 60/180,312
| PRIOR FILING DATE: 2001-05-26
| PRIOR FILING DATE: 2000-05-26
| PRIOR FILING DATE: 2001-00-04
| PRIOR FILING DATE: 2001-01-30
| PRIOR FILING DATE: 2001-01-
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Sequence 16984, Application US/09864761 Patent No. US20020048763A1
                                                               GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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SOFTWARE: Annomax Sequence I
SEQ ID NO 16984
LENGTH: 243
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: OFFOSINES in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
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US-10-363-345A-17160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
14.4%; Score 91.8; DB 18; Length 1128;
Best Local Similarity 77.6%; Pred. No. 1.1e-15;
Matches 111; Conservative 0; Mismatches 32; Indels 0;
                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                               SEQ ID NO 17160
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| Sequence 17159. Application US/10363345A
| Publication No. US20040234960A1
| GENERAL INFORMATION:
| APPLICANT: Alexander Olek
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| APPLICANT: Christian Piepenbrock
| TITLE OF INVENTION: Mcthod for determining the degree of methylation of defined
| TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3|
| TITLE OF INVENTION: Cytosines US/10/363,345A
| CURRENT APPLICATION NUMBER: US/10/363,345A
| CURRENT PILING DATE: 2003-03
| NUMBER OF SEQ ID NOS: 40712
| SEQ ID NO 17159
| LENGTH. 11:0
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US-10-363-345A-17159
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; OTHER INFORMATION: SWISSPROT HIT: P31157, EVALUE 1.50e+00; OTHER INFORMATION: EST_HUMAN HIT: BE731965.1, EVALUE 1.00e-112 US-09-864-761-16984
                                                                                                      Score 239.8; DB 9; Length 243; Pred. No. 7.3e-57; 0; Mismatches 2; Indels 0
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ORGANISM: Artificial Sequence
                                                                                                Query Match
Best Local Similarity 99.2°
Matches 241; Conservative
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US-10-363-345A-17159
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Sequence 17157, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION.
APPLICANT: Alexander Olek
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461 TTGGAGGCGGCGTTAGGGTTTTTCGTGAAGAAGTCGCGGTTTCGCGGATTACGGTTTTGG 402
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US-10-363-345A-17157
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75.7%; Pred. No. 5.7e-14;
tive 0; Mismatches 34; Indels
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Matches 106; Conservative
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US-10-363-345A-17157/c
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RESULT 4
US-10-363-345A-17160/c
US-10-363-345A-17160/, Application US/10363345A
; Publication No. US20040234960A1

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ORGANISM: Zea mays
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Dants and Uses Thereof for Plant Improvement
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)8
CURRENT APPLICATION NUMBER: US/10/425,114
UNDMER OF SEQ ID NOS: 73128
SEQ ID NOS: 73128
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                                                                                             Sequence 17158, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of def
TITLE OF INVENTION: Oytosines in genomic DNA in the sequence context of 5'
CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT APPLICATION NUMBER: US/10/363,345A
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 17158
LENGTH: 1128
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US-10-363-345A-17158
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7.2%; Score 46.2; DB 17; Length 1770;
Best Local Similarity 51.2%; Pred. No. 0.0053;
Matches 108; Conservative 0; Mismatches 103; Indels 0;
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US-10-425-114-25086
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Publication No. US20040034888A1
  401 AACCTCACGAAACTCGCAAA 382
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Sequence 165209, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION: US20040214272A1
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Dlants
; TITLE OF INVENTION: 0163223
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 165209
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JEQUENCE 6, Application US/09802127

Sequence 6, Application US/09802127

Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 6, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 7, Sequence 8, Sequence 7, Sequence 8, Sequence 8, Sequence 7, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8, Sequence 8,
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No. 0.0053; Matches 108; Conservative 0; Mismatches 103;
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US-10-425-115-165209
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US-09-764-868-1501
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Patent No. US20020045212A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gluckemann, Maria Alexandra
APPLICANT: Meyers, Rachel
TITLE OF INVENTION: No. US0020045212A1el Human GTPase Activator Proteins
FILE REFERENCE: 035800/158994
CURRENT APPLICATION NUMBER: US/09/802,127
CURRENT APPLICATION NUMBER: 60/105.23
PRIOR APPLICATION NUMBER: 60/105.29
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53.3%; Pred. No. 0.055;
iive 0; Mismatches 79; Indels 0
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Patent No. US20020168711A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                  Score 42.6; DB 9; Length 3 Pred. No. 0.054; 0; Mismatches 79; Indels
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 3391
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Best Local Similarity 53.3%;
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ORGANISM: Homo sapiens
US-09-802-127-6
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US-09-764-868-1501
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                                   SEQ ID NO 6
LENGTH: 3018
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Pred. No. 0.056;
0; Mismatches 79; Indels 0;
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1501
LENGTH: 5968
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Publication No. US20030082758A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P.ZZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
Prior Application removed - See File Wrapper or Palm
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Pred. No. 0.056;
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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Matches 90; Conservative
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, ORGANISM: Homo sapiens
US-10-103-313-619
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Matches 90; Conserv
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US-10-437-963-13512/c
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Best Local Similarity 49.55
Matches 108; Conservative
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 13512
LENGTH: 3368
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No. 0.065; Live 0; Mismatches 23; Indels
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APPLICANT: Steeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Control, Nevin
APPLICANT: Rumble, Anand
APPLICANT: Murison, Greg
TITLE OF INVENTION: Compositions Isolated From Stromal Cells
FILE REFERENCE: 11000.1037c3
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Patent No. US20020058335A1
GENERAL INFORMATION:
                          Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
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Best Local Similarity 70.9
Matches 56; Conservative
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Matches 106; Conservative
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ORGANISM: Mouse
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1. (Dases 1 to 790)
1. (M.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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//db xref="teaxon:90077400"
/clone="CSODIO27Y400"
/clone="ICSODIO27Y401"
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/clone_ilb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-Oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                         BX357315
BX344130
BX345009
BX337459
BX387069
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BX343795
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BX366004
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Contact: Genoscope
Length 790;
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Pred. No. 5.4e-135;
0; Mismatches 1;
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BX358526
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Gaps

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240 244 304

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BX365974 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI031YB04 5-PRIME, mRNA sequence.

BX365974.2 GI:46288863
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/mol type="mRNA"
/db xref="taxnA"
/db xref="taxnA"
/clone="CSODIO34YP24"
/clone="CSODIO34YP24"
/clone="Type="PIACENTA COT 25-NORWALIZED"
/clone="lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="lib="taxnad cDNA was primed with a NotI-oligo(dT)
/primer. Five prime end enriched, double-estrand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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There is a virtual cDNA representing this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CS5AA014ZD04RM1&c=7348.r. Location/Qualifiers
                                                                                                                                                                                                                                                                                           Length 826;
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Pred. No. 5.5e-135;
0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 638; Conservative 0
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Contact: Genoscope Genoscope Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Ist strand cDNA was primed with a NotI-oligo(dT) primer. Primer Primer end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX387234 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSODI034YP24 5-PRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
Unpublished (2001)
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                                               TIGAGIACCCCIAACCCIGAIAACCAGGIGACCAICAAG 639
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KEYWORDS
SOURCE
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JOURNAL
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                                                                                                                                                                                       Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NoLI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                 information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CS2BAX12ZF12_AX21ZH4_1&c=7348.r. Location/Qualifiers
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                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                             2003 this sequence version replaced gi:30370960
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                                                                                                                             normalization
                                                                                                          and Polayes, D.
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Pred. No. 5.5e-135;
0; Mismatches 1;
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                                                                                       1 (bases 1 to 866)
Li,w B., Gruber,C., Jessee,J. a
Full-length cDNA libraries and
Unpublished (2001)
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/db_xref="taxon:9606"
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larity 99.8%; Pre
Conservative 0;
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On May 13, 2003 this sequence version replaced gi:30615118.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVBORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BX403263 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI075YH10 5-PRIME, mRNA sequence.
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1 (bases 1 to 867)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer: Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Pred, No. 5.5e-135;
0; Mismatches 1;
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/clone="CS0DI075YH10"
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BX344975 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO05YP06 5-PRIME, mRNA sequence.
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(Liases 1 to 872)

Li.W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30346327.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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                                                                                            Score 637.4; DB 5;
Pred. No. 5.5e-135;
0; Mismatches 1;
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2. (contact: Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage - Centre National de Sequencage - Centre National de Sequencage - Structure Mational de Sequencage - Centre National de Sequencage - Structure Mational de Sequencage - Centre National de Sequencage - Alusta de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Management de Managemen
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BX365998 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI074Y001 5-PRIME, mRNA sequence.
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/tissue type="TPACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note===strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
                              GAGGAGGCACCACTGCTCCCCAGAACCCACTGCAGGCAGAGGCCACACAACATGGATGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                          _type="mRNA"
_xref="taxon:9606"
                                                                                                                                                                                                                                        /clone="CS0DI005YP06"
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
BX198022 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA EX198022
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Catarrhini; Hominidae; Homo
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0; Mismatches 1;
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Mammalia; Butheria; Primates; Cat
1 (bases 1 to 900)
Li, W.B., Gruber; C., Jessee, J. and
Full-length cDNA libraries and no
Unpublished (2001)
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Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSFORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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division of Invitrogen. This sequence belongs to sequence cluster
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COT 25-NORMALIZED Homo sapiens cDNA
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDDA libraries and normalization Unpublished (2001)
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/tissue type="PLACENTA" COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Not1-oligo(dT)
/note="lst strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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larity 99.8%; Pred. No. 5.5e-135;
Conservative 0; Mismatches 1; Indels 0;
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/db_xref="taxon:9606"
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936 bp mRNA linear EST 26-APR-2004
BX381620 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI068YE01 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                       CTGGAGGCGCGCTAGGGCTCCCCGTGAAGAAGCCGCGGCTCCGCGGGACCACGGCCTGGG 128
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 936)
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primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
digested with Not I and cloned into the Not I and ECOR V
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Pred. No. 5.5e-135;
0; Mismatches 1;
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BX381620.2 GI:46570758
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REFERENCE

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/db_xref="taxon:9606"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                   On May 8, 2003 this sequence version replaced gi:30443700 Contact: Genoscope
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 5.5e-135;
0; Mismatches 1;
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Matches 638; Conserv
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엄 ð 셤

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On May 8, 2003 this sequence version replaced gi:30452951.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Brail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWWSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX381477 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO66YK17 5-PRIME, mRNA sequence.
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/note="lst strand cDNA was primer. Five prime end enriched, double-estrand cDNA was
digested with Not I and cloned into the Not I and SCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 960)
                                                                                      GAGGAGGAGGACGCTCCCCAGAACCCACCTGCAGAGCCAGAGCTACAACATGGA
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                                                       GAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGGATTGGCCAGCACCTTG
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Pred. No. 5.5e-135;
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/db_xref="taxon:9606"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

E. 1, Wases I to 947)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
L. Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30376366.
Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Z. rue Gaston Cremieux, CP 5706 - 91657 FWRX cedex - FRANCE
Email: seqref@Genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
       612
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BX359737 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI060YF04 5-PRIME, mRNA sequence.
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
CAGGAGGTTACTCCCTTGCTGCTGGAGCTGCAGAATTGGTCCACGCAACC
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larity 99.8%; Pred. No. 5.5e-135;
Conservative 0; Mismatches 1;
                                                TTGAGTACCCCTAACCCTGATAACCAGGTGACCATCAAG
                                                                              'organism="Homo sapiens"
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'db_xref="taxon:9606"
'clone="CS0DI060YF04"
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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BX336623
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                          There is a virtual cDNA representing this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CSODIO10DB01QP1&c=7348.r. Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqret@genoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX356306 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI010YD02 5-PRIME, mRNA sequence.
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BX356306.2 GI:46303698
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373 420 433 480 493 540 553

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Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope. Cns. fr. Web: www.genoscope.cns. fr
Email: seqrefégenoscope. Cns. fr. Web: www.genoscope. Cns. fr
Ist strand CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                  973 bp mRNA linear EST 27-APR-2004
BX379676 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
CLONE CSODI037XE05 5-PRIME, mRNA sequence.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 973)
1. (J. W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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Pred. No. 5.5e-135;
0; Mismatches 1;
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/db_xref="taxon:9606"
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Contact: Genoscope
Contact: Genoscope
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
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into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
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                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 91)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Lissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  373 AGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                  information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CSODI030AH10QP1&c=7348.r. Location/Qualifiers
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Pred. No. 5.5e-135;
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99.8%; Pred. 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODI030YO19"
  GI:46272943
                                           sapiens (human)
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This invention relates to polynucleotide sequence PSEC137, which encodes a buman proliferation differentiation factor protein. Included in the invention is a vector containing the CDNA sequence, a transformant containing the vector, and a process for producing the protein. The protein together with its encoded DNA and antisense DNA are used in drugs to maintain the haematopoietic function. The present sequence represents the human proliferation differentiation factor protein amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proliferation-differentiation factor protein encoded by PSEC137 cloned from human cDNA library, being hematopoietic factor for inducing differentiation of blood cells, used to maintain hematopoietic function.
                                                                                                                                                                                                                                                                                                                    Human; proliferation differentiation factor; haematopoietic function
Abb643375
Abb64387
Abb18375
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Ada5745
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Add01162
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                                 ADA57458
AAB38427
ADD71122
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AAU01623
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ABB08164
ABG30717
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ABM81720
AAB90819
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AAB94325
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99US-0159586P
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N-PSDB; AAF29348
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18-OCT-1999;
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AAB49765;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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AAB88419. Included in the invention are primers AAF932917 - AAF94295 and
AAF62232 - AAF62235 which are used to isolate the cDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polymucleotide sequences can be used in gene
therapy. The polymucleotide sequences and the proteins they encode may be
cused in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
cucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect
and quantitate the presence of similar nucleic acid sequences in samples.
They may also be used to study the expression and function of secretory
proteins/membrane polypeptides and their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
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                                                                                                                         87 AAMTPGNTTPPRIPEVTPLRELQKLPGLASTTLSTPNPDTQASASPDPRPLREEEEARL 146
                                                                                                                                                                   147 LPRTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 206
                                                                                                    AAMTPGNITTPPRIPEVIPLRIELOKLPGLASITLSIPNPDIQASASPDPRPLREEEBARL 120
                                                                                                                                                     LPRIHLQAELHQHGCWIVTEPAALIPGNATPPRIQEVIPLLLELQKLPELVHATLSIPNP 180
                                                                          LPVKKPRLRGPRPGSLTRLAEVSASPDPRPLKEBEBAPLLPRTHLQAEPHQHGCWTVTEP 86
                                                  LPVKKPRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEP
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                           Gaps
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gene therapy or as candidate target molecules in drug development
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Pred. No. 1.6e-75;
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             100.08;
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                                                                                                                                                                                                                86
against them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumatoid arthritis and diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM13752 standard; protein; 81 AA.
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-0063366.
; 2000US-0234687P.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNQVTIK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNOVTIK 213
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                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 187; Conserv
                                                                                                                                                                                                        Sequence 571 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157278-A2.
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21-SEP-2000; 2
27-SEP-2000; 2
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30-JUN-2000;
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Gaps ö

81;

Score 430; DB 4; Pred. No. 8.3e-29; ; Mismatches 1.

9

gene expression.

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22 VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRL
                                                                                                                                    1 VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEVTPLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide #187 encoded by probe for measuring placental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen W, Rank DR,
                                                                                                                                                                         ELOKLPGLASTTLSTPNPDTQ 102
                                                                                                                                                                                               ELOKLPGLANTTLSTPNPDTQ
                                                                                                                                                                                                                                                                                                           AAM26150 standard; protein; 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236399P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JAN-2001; 2001WO-US000663.
                       43.2%;
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                             Conservative
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                       Query Match
Best Local Similarity
Matches 79; Conserv
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nes 79; Conserv
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Matches
                                                                                                                                                                                                                                                                                         AAM26150
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by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                           VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEVTPLRL 60
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #191 encoded by human foetal liver single exon probe.
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                                                                                                                                                                                                                Length 81;
                                                                                                                                                                                                                                                                                       VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTP
                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                            Score 430; DB 4;
Pred. No. 8.3e-29;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB32685 standard; peptide; 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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                                                                                                                                                                                                              43.2%;
97.5%;
                                                                                                                                                                                       Query Match
Best Local Similarity 9/...
Best Toy, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                         Sequence 81 AA;
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03-AUG-2000; 2
21-SEP-2000; 2
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ABB3268 RESULT

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Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                             The present invention relates to single exon nucleic acid probes (SENP: see AAI1115-AA157546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRL
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1; Mismatches 1: r...
                                                                            Claim 27; SEQ ID NO 26419; 654pp; English
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                              gene expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                         43.2%;
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Sequence 81 AA;

ELOKUPGLASTILSTPNPDTQ 102

82

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61 ELQKLPGLANTTLSTPNPDTQ

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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from muna breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents after greater diversity of probes for measuring microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a peptide information from genomic sequence. The present sequence is a peptide concoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed sequence in sequence data for this patent did not form part of the printed sequence.
                                                                                                                                              Human peptide #177 encoded by breast cell single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes.
                                                                                                                                                                                      Human; microarray; single exon probe; gene expression; breast; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a spatially-addressable set of single exon
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Best Local Similarity 97.5%; Pred. No. 8.3e-29;
Matches 79; Conservative 1; Mismatches 1; Indels
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at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen W, Rank DR;
                                ABB27526 standard; peptide; 81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0180312P
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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                                                                                                                                                                                                                                                                                          WO200157271-A2
                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                             01-FEB-2002
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                                                                         ABB27526;
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                                                                                                                                                                                                                cancer.
RESULT
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                                                                                                                                                                        Protein #175 encoded by probe for measuring heart cell gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single exon nucleic acid probes for analyzing gene expression in human hearts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRL
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                                                                                                                                                                                                Human, gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
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Pred. No. 8.3e-29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; SEQ ID NO 19946; 530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rank DR
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          61 ELOKLPGLANTTLSTPNPDTQ 81
                                                                                           ABB18176 standard; protein; 81 AA
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.2%;
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                                                                                                                                                 23-JAN-2002 (first entry)
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Best Local Similarity 97.5
The conservative 79; Conservative
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                                                                                                                                                                                                                                                                                           WO200157274-A2.
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                                                                             ABB18176
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Gaps

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81

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22 VSASPDPRPLKEEEEAPLLPRIHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRL

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Sequence 81 AA;
                                                WO200157275-A2
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                              Homo sapiens
                                                                                                          04-FEB-2000;
26-MAY-2000;
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                                                                   09-AUG-2001
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                                                                                                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                            probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEVTPLRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human brain expressed single exon probe encoded protein SEQ ID NO: 25612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSASPDPRPLKEBEBAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma.
                                                                                                                                                                                                                                                                                                                                                                                                                    present invention provides a number of single exon nucleic acid
                                                                                       Human bone marrow expressed probe encoded protein SEQ ID NO: 26191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 430; DB 4;
Pred. No. 8.3e-29;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                          B,
                                                                                                                                                                                                                                                                                                                                                                            gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                           Rank
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                            AAM65885 standard; protein; 81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 81 AA
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                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                              26-MAY-2000; 2000US-0207456F-
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-023366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-0236359P.
                                                                                                                                                                                                                                                                         27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000668
                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                          Hanzel DK,
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 81 AA;
                                                                                                                                                           WO200157276-A2
                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-NOV-2001
                                                                   06-NOV-2001
                                                                                                                                                                                09-AUG-2001
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                                                AAM65885
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Best Local &
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                AAM65885
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         RESULT
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Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEVTPLRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 430; DB 4;
Pred. No. 8.3e-29;
1; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human liver peptide, SEQ ID No 26188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABG47540 standard; peptide; 81
                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                             30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEE-2000; 2000US-0234687P.
27-SEE-2000; 2000US-0236359P.
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                                                                                                                                                                                          30-JAN-2001; 2001WO-US000667
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Best Local Similarity 97.5%,
Conservative
T9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanzel DK,
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(see AA10010-AA11067). The present sequence is a peptide encoded by one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe bybridses at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing predicting, diagnosing, grading, staging, monitoring and prognosing alseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development inflammatory diseases of the breast, fibrocystic changes, proliferative this patent did not form part of the printed specification, but was ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                        Novel single exon nucleic acid probe used to measuring gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSASPDPRPLKEEEEBAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEVTPLKL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human peptide encoded by genome-derived single exon probe SEQ ID 25185.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary hatlocytosis; lymphangioleleiomyonchosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.2%; Score 430; DB 4;
97.5%; Pred. No. 8.3e-29;
tive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 10237; 322pp; English.
                                                                                                                                                                          Chen W, Rank DR;
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                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG35520 standard; peptide; 81
                                                             27-SEP-2000; 2000US-0236359P.
                  2000US-00632366.
2000US-0234687P.
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Matches 79; Conservative
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                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                 WPI; 2001-476286/51
                                                                                                                                                                                                                                                                                 human breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200186003-A2
                  03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                        Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ASG47348 ASG59910 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification have sobtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoded by probe for measuring human breast gene expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 430; DB 4; Length 81
Pred. No. 8.3e-29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                  Claim 27; SEQ ID NO 26188; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                 Chen W, Rank DR,
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                                                                           03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0235.99P.
04-OCT-2000; 2000GB-00024263.
                                    2000US-0207456P.
2000US-00608408.
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97.58;
               2000US-0180312P
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Best Local Similarity 97.5
Matches 79; Conservative
                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                            WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200157270-A2
                                    26-MAY-2000;
                                                      30-JUN-2000;
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AAMO1497

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ABU53252
                                                                             The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived comprising single exon mucleic acid probes any or the 1281 or the 1281 or the 1281 or the 1281 or the 1281 or the 1281 or the 1281 or the 1281 or complements or the 1281 open reading frames derived from the 1281 or probes. Also included are a microarray comprising the novel set of probes or the 1281 open reading frames derived from the 1281 or probes. Also included are a microarray comprising the novel set of probes or the burning comprising of a caids derived from human lung comprising of a caids derived from human lung microarray comprising (a) conteacting the array with a caid derived from human lung manual babel detectably bound to each probe of the array identifying exons in a eukaryotic genome, comprising (a) array; identifying exons in a eukaryote lung manual comprising (a) algorithmically predicting a least one exon from genomic sequences of the enkaryote; and (b) measuring the albel detectably bound to each probe of the example of the exons in a eukaryote lung manual or detectably a lagorithmically predicting apecific hypitidisation of detectably a ladoritifying exons from genomic sequences of the the above mentioned microarray; assigning exons to a single exon probe, and the above mentioned microarray; assigning exons to a single exon in geveral comprising (a) identifying exons in the tissues and/or cell types using phyridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons should be assigned to a single gene; a peptide comprising on analysis, and for identifying exons in the gene; particularly using human derived manual dorithmic pattern of analysis, and for identifying exons in an gene, particularly using human concer, chronic obstructive pulmonary haemosiderosis, pulmonary haemosiderosis, pulmonary haemosiderosis, pulmonary haemosiderosis, pulmonary hypertension and hyaline menomen as a peptide/prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VSASPDPRPLKEEEERAPILPRTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEVTPLRL 60
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                                                                                                                                                                                                                                                                                                                           Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 8.3e-29;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 27; SEQ ID NO 25185; 634pp; English.
                                                                                                                                                                                                                            Rank DR;
                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                            Chen W,
                                                                        21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
2000US-0207456P.
2000US-00608408.
                                                   03-AUG-2000; 2000US-00632366.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.2%;
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Best Local Similarity 97.57
Period 79; Conservative
                                                                                                                                                                                                                            Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                             WPI; 2002-114183/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 81 AA;
                       30-JUN-2000;
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Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies.

(GEHU-) GERMAN HUMAN GENOME PROJECT.

WPI; 2001-327840/34.

Wiemann S;

99US-0156503P 99US-0149499P

18-AUG-1999; 28-SEP-1999;

18-AUG-2000; 2000WO-IB001496.

WO200112659-A2.

22-FEB-2001,

Homo sapiens.

Example III; Page 892; 1095pp; English.

Human; gene therapy; vaccine; disease treatment; detection.

Human testes-derived DKFZphtes3_4019 homologue #1.

(first entry)

14-APR-2003

ABU53252;

ABU53252 standard; protein; 546 AA.

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from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by them may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. The products of the invention may also be used to identify modulators of expression and activity and to down regulate expression and activity. The antibodies of the invention may also be used as diagnostic agents for detecting the presence of polypeptides in samples. This sequence represents a homologue of a polypeptide described in the disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТККРАРТАРКЕРАРТТРК 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 RIPEVTPLRIELØKLPGLASTILSTPNPDTQASASP----DPRPLREEEEARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ЕТАРТТРККІТРТТРЕКІАРІТРЕКРАРТТРЕЕГАРТТРЕЕРТРТРЕЕРАРТТРКАААР 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT------PGNTTPP 71
This invention describes novel polynucleotides and polypeptides isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NTPKEPAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.5%; Score 144; DB 4; Length 546;
Best Local Similarity 28.4%; Pred. No. 0.001;
Matches 50; Conservative 11; Mismatches 97; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 546 AA;
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ELOKLPGLASTTLSTPNPDTO 102 ELOKLPGLANTILSTPNPDTQ 81

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The present sequence is that of novel human extracellular messenger (EXMES) Incyte ID NO: 7513017CD1 polypeptide. The protein shows homology to human megakaryocyte stimulating factor. The invention provides EXMES polynucleotides and polypeptides, as well as expression vectors, host cells, antibodies, agonists and antagonists, and methods for diagnosing, treating or preventing disorders associated with aberrant expression of EXMES, especially autoimmune and inflammatory disorders, cell proliferative disorders and endocrine disorders, e.g. adult respiratory distress syndrome, allergy, anaemia, erythroblastosis foetalis, Crohn's distress syndrome, allergy, anaemia, erythroblastosis foetalis, Crohn's osteoporosis, pancreatitis, psortasis, viral, bacterial, fungal, osteoporosis, protozoal or helminthic infections, cancers, autoimmune thyroiditis, cretinism, Plummer's disease or thyroid carcinoma. Embodiments also provide methods for using the purified EXMESs and/or continuity and polynucleotides for facilitating the drug discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New extracellular messengers and nucleic acids, useful for diagnosing, treating or preventing e.g. allergies, anemia, Crohn's disease, diabetes mellitus, myasthenia gravis, osteoporosis, psoriasis, cancers or autoimmune thyroiditis.
                                      Human; extracellular messenger; EXMES; respiratory-gen.; antiallergic;
antialathmatic; antialfammatory; antidabetic; neuroprotective;
muscular-gen.; antiarthritic; osteopathic; hepatotropic; antipsoriatic;
virucide; fungicide; antiparasitic; protozoacide; antihelminthic;
                                                                                                                                                                                                                                                            29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elliott VS, Khare R, Tran UK, Swarnakar A, Marquis JP;
Richardson TW, Emerling BM, Lindquist EA, Chawla NK, Ramkumar J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      process, including determining of efficacy, dosage, toxicity and pharmacology, and for investigating the pathogenesis of diseases and medical conditions.
                                                                                                                                                                                                                                                              or
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                                                                                                                                                                                                                                                            24,
                                                                                                                                                                                                                 1. .29
/label= Signal_peptide
/note= "Spans residues 1 to 18, 20,
according to identification method"
Human extracellular messenger (EXMES) polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%; Score 144; DB 8; 28.4%; Pred. No. 0.0026; iive 11; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 59; SEQ ID NO 4; 165pp; English
                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2002; 2002US-0400810P.
19-SEP-2002; 2002US-0412197P.
04-OCT-2002; 2002US-0416004P.
08-NOV-2002; 2002US-0424662P.
                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2003; 2003WO-US024084
                                                                                                                   cytostatic; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-157116/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (INCY-) INCYTE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-157116/:
N-PSDB; ADK67916.
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                                                                                                                                                                                                                                                                                                                 WO2004013292-A2
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       12-FEB-2004
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                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee SY;
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SASPDPRPLKEBEEAPLLPRTHLQAEPHOHGCWTVTEPAAMT----

Conservative

20; 23

Matches

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Local Similarity

97; Indels

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481 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPAPTTPEEPAPTTPKAAAP 540
                                                                                                                                                                                                                                                        Human, sheep, pig, cow, fruit fly, yeast; hamster; macaque; horse,
tomato, monkey, dog, sea urchin, expressed sequence tag; EST;
diagnostics, forensic test, gene mapping; genetic disorder; biodiversity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, biodiversity and for nutritional purposes. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIPEVIPLRIELOKLPGLASTILSTPNPDTQASASP----DPRPLREEEEARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615 БТАРТТРККІТРТТРЕКІ,АРТТРЕКРАРТТРЕВІЛАРТТРЕВРТРТРЕВРАРТТРКАДАР 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---PGNTTPP 71
                                            AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       541 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТЬКЕРАРТТРККРАР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.5%; Score 144; DB 4; 28.4%; Pred. No. 0.0027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                                               Human EST encoded protein SEQ ID NO: 1847.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merhman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 1198-1201; 1275pp; English.
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J, Werh
                                                                                                                                            AAM24322 standard; protein; 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SBP-2000; 2000US-0063870.
                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-2001; 2001WO-US002687.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou P, (
A, Zhang i
                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                     therapy; nutrition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drmanac RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1299 AA;
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N-PSDB; AAH98981
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                                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50;
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                                          128
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Matches
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                                                                                                                 RESULT 15
                                                                                                                               AAM24322
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Tue Feb 22 09:49:21 2005

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675 NTPKEPAPTTPKEPAPTTPKEPAPTTPKGTAPTTLKEPAPTTPKKPAP 730 Search completed: February 18, 2005, 23:56:01 Job time : 172 secs

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us-10-030-225-2_copy_27_213.rai

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ATTORNEY AGENT INFORMATION:
NAME: CREAT, LUGATH
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 941 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 104, App
Sequence 44, Appl
Sequence 42, Appl
Sequence 142, Appl
Sequence 50, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 78, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 10827, A
Sequence 10827, A
Sequence 10827, A
Sequence 1258, Appl
Sequence 1258, Appl
Sequence 1258, Appl
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Sequence 137, App
Sequence 142, App
Sequence 137, App
                                                                                                    February 18, 2005, 23:50:51; Search time 43 Seconds (without alignments) 324.637 Million cell updates/sec
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                                                                                                                                                                          Title:
US-10-030-225-2_COPY_27_213
Perfect score: 995
Sequence: 1 I.PVKKPRLRGPRPGSLTRLA.......PELVHATLSTPNPDNQVTIK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
Sequence
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 · Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-757-022B-14
US-07-757-022B-84
US-07-757-022B-104
US-07-757-022B-104
US-07-757-022B-42
US-07-757-022B-42
US-07-757-022B-142
US-07-757-022B-160
US-07-757-022B-60
US-07-757-022B-60
US-07-757-022B-40
US-07-757-022B-40
US-07-757-022B-52
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US-08-818-111-137
US-09-056-556-142
US-09-072-596-137
                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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Match Length
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                                                                                                                                                                                                                                                   Scoring table:
                                                                   OM protein
                                                                                                                                                                                                                                                                                                                                                                              Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                         Searched:
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                                                                                                      Run on:
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	-525	ting Factors n #1.25
09-072-967- 09-518-092- 08-96-865- 09-129-668- 09-949-016- 09-949-016- 09-949-016- 09-949-016- 08-45-594- 09-949-016- 08-45-594- 09-949-016- 08-949-016- 08-949-016- 08-949-016- 09-96-96-96-96-96-96-96-96-96-96-96-96-96	US-09-107-532A ALIGNMENTS	In US/07757022B Thomas G. Stephen C. Katherine Rodney M. Megakaryocyte Stimulating 1 143 183 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 143 Institute, Inc. 144 Institute, I
11.2 10.9 10.9 10.9 10.8 696 10.8 10.6 10.6 10.6 10.6 10.6 10.6 10.6 10.6	4.	plication 142 ATION: Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St Glasher, St ATION: ST ATION: ST A
28 1111.332 1008.5334 1008.5334 1007.5834 1008.544 1008.544 1008.544 1008.544 1008.544 1003.554 1003.5	10	RESULT 1 Sequence 14, Application Sequence 14, Application PAPLICANT: General APPLICANT: General APPLICANT: Turner, APPL

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ZIP: 02140
  US-07-757-022B-84
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                                                                                                                                                                                                                    356 ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТККРАРТАРКЕРАРТТРК 415
                                                                                                                                                                                                                                                                                                         416 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAP 475
                                                                                                                                                                                                                                                                72 RIPEVIPLRIELQKLPGLASTILSTPNPDIQASASP----DPRPLREEEBARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                                                                       128 AELHOHGCWTVTEPAALT---PGNATPPRIQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                476 ИТРКЕРАРІТРКЕРАРІТРКЕРАРІТРКЕТАРІТРКСТАРІТІКЕРАРІТРККРАР 531
                                                                                                                                  18; Gaps
                                                                                      Length 941;
                                                                                  14.5%; Score 144; DB 4; Length 94.
28.4%; Pred. No. 2.4e-05;
trive 11; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION S30
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTOMENYAGEN: INFORMATION:
                                                                                                                                                                           23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Genetics Institute, Inc
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cserr, Luann
RECISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 84, Application US/07757022B Patent No. 6433142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP. 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
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(617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1022 amino acids
                                                                                                                             50; Conservative
                  ; MOLECULE TYPE: protein US-07-757-0228-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                  Query Match
Best Local Similarity
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-07-757-022B-84
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497 ETAPTTPKKLIPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTPEEPAPTTPKAAAP 556
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                                                                                                        ---- PGNTTPP
                                                                                                                                                                                                                                                                                                        128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLBLQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                          557 NTPKEPAPTTPKÉPÁPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 612
                                                       18;
  14.5%; Score 144; DB 4; Length 1022; 28.4%; Pred. No. 2.7e-05; Live 11; Mismatches 97; Indels 18
                                                                                                      23 SASPDPRPLKEEEEAPLLPRTHLQAEPHOHGCWTVTEPAAMT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: LOSSING-DOS OPERATING SYSTEM: PC-DOS/NS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/757,022B FTIING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19910910
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Patent No. 643342
| GENURAL INFORMATION:
| APPLICANT: Gener Thomas G.
| APPLICANT: Turner, Ketherine
| APPLICANT: Turner, Katherine
| APPLICANT: Hewick, Rodney M.
| ITILE OF INVENTION: Megakaryocyte SI
| NUMBER OF SEQUENCES: 143
| CORRESPONDENCE ADDRESS:
| ADDRESSEB: Genetics Institute, Inc.
| STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-757-022B-74
; Sequence 74, Application US/07757022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMINICATION: TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1038 amino acids
TYPE: AMINO ACID
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
Query Match
Best Local Similarity
Matches 50; Conserv
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18; Gaps

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72 RIPEVIPLRIELOKLPGLASTILSTPNPDIQASASP----DPRPLREEEEARLLPRTHLQ 127
                                                                                                                                                                                                  524 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAP 583
                                                                                                                                                                                                                                                     128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                584 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТКЕРАРТТРККРАР 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97; Indels 18;
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14.5%; Score 144; DB 4; Length 1140;
Best Local Similarity 28.4%; Pred. No. 3.1e-05;
Matches 50; Conservative 11; Mismatches 97; Indels 1
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Ratherine
APPLICANT: Turner, Ratherine
APPLICANT: Turner, Ratherine
APPLICANT: Turner, Ratherine
APPLICANT: Turner, Ratherine
APPLICANT: Gooden
APPLICANT: Turner, Ratherine
APPLICANT: Gooden
APPLICANT: Gooden
APPLICANT: Turner, Ratherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge Park Drive
CITY: Cambridge
STATE: Massach...
                                                     23 SASPOPRPLKEBEBAPLLPRTHLQAEPHQHGCWTVTEPAAMT-----
       97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
CONTRANT APPLICATION NATA:
APPLICATION NATA: US/07/757,022B
FILING DATE: 19910910
       11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502

FILING DATE: 18-JAN-1991

PRIOR APPLICATION NUMBER: US 07/546,114

FILING DATE: 29-DUN-1990

PRIOR APPLICATION NUMBER: US 07/457,196

FILING DATE: 29-DEC-1989

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901

FILING DATE: 08-AUG-1989

ATTORNEY/AGENT INFORMATION:
NAME: CSERT, LUBING NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 104, Application US/07757022B
; Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5190
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1140 amino acids
       50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)876-5851
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMINO ACID
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     Matches
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                                                                                                                                  481 ЕТАРТТРККІТРІТРЕКІАРІТРЕКРАРІТРЕЕЛАРІТРЕЕРТРІТРЕВРАРІТРКАЛАР 540
                                                                                                                                                                                                  72 RIPEVIPLRIBLOKLPGLASTILSTPNPDIQASASP----DPRPLREEBEARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                128 AELHOHGCWTVTEPAALT --- PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                541 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 596
  14.5%; Score 144; DB 4; Length 1038; 28.4%; Pred. No. 2.8e-05; Live 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.5%; Score 144; DB 4; Length 1049; 28.4%; Pred. No. 2.8e-05;
                                                                                                 23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILNG DATE: 19910910
CLASSIFICATION: 530
RIGOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
PRIOR APPLICATION NUMBER: US 07/57,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/57,196
FILING DATE: 29-DEC-1989
FILING DATE: 28-DEC-1989
RILING APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-NUG-1989
ATPONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31,822
ER: GI 5190
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-757-022B-58
; Sequence 58, Application US/07757022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Geener, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc; NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1049 amino acids
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Cambridge
STATE: Massachusetts
Query Match |
Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6433142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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421 TTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPK 480
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                             Patent No. 6433142
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
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TELEFAX: ('
                                                                                                                                                                                                                                              RESULT 7
US-07-757-022B-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                           555 ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТТККРАРТАРКЕРАРТТРК 614
                                                                                      72 RIPEVIPLRIELQKLPGLASTILSTPNPDTQASASP----DPRPLREEEEARLLPRIHLQ 127
                                                                                                                                 615 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕЕГАРТТРЕЕРТРЕЕРАРТТРКАААР 674
    ---- PGNTTPP 71
                                                                                                                                                                                                                       675 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТІКЕРАРТТРККРАР 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- PGNTTPP
                                                                                                                                                                            128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY

ZIF: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B

TILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 SASPDPRPLKEEEEAPLLPRTHLQAEPHOHGCWTVTEPAAMT-
SASPOPRPLKEEEEAPLLPRTHLQAEPHOHGCWTVTEPAAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

A PAPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: GBETT INFORMATION:
NAME: CBETT LAID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                             Sequence 44, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 28.49
Matches 50, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                    RESULT 6
US-07-757-022B-44
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72 RIPEVIPLRIELOKLPGLASTILSTPNPDIOASASP----DPRPLREEEEARLLPRIHLQ 127
                                                  481 ЕТАРТТРККІЛРТТРЕКІАРТТРЕКРАРТТРЕВІЛАРТТРЕВРТРТТРЕВРАРТТРКАЛАР 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                        541 МТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТГКЕРАРТТРККРАР 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFILING DATE: 19910910
CLASSIFICATION UNDERE: US/0//75/,0228
FRIOR APPLICATION DATE: 19910910
FRIOR APPLICATION DATE: B-JAN-1991
FRIOR PAPLICATION DATE: 18-JAN-1991
FRIOR APPLICATION DATE: 29-JUN-1990
FRICR APPLICATION NUMBER: US 07/45/,196
FILING DATE: 29-DEC-1989
FRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022
FTIING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION: NIPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    ; Sequence 42, Application US/07757022B
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Geener, Thomas G. APPLICANT: Clark, Scephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1311 amino acids TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / MOLECULE TYPE: protein US-07-757-0228-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
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524 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAP 583
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMINICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                         RESULT 9
US-07-757-022B-50
Sequence 50, Application US/07757022B
; Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 1314 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02140
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72 RIPEVIPLRIELOKLPGLASTILSTPNPDIQASASP----DPRPLREEEBARLLPRIHLQ 127
                        RIPEVIPLRIELOKIPGLASTILSTPNPDIQASASP----DPRPLREEEBARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT------PGNTTPP 71
                                                                                                              582 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 637
                                                                        128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 144; DB 4; Length 1313; 28.4%; Pred. No. 3.7e-05;
                                                                                                                                                                                                                  APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
URRENT APPLICATION DATA:
APPLICATION UNMER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Pred. No. 3.7e 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
RICA PAPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
RICA APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
RICA APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
RICA APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        E: Genetics Institute, Inc. 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: CBET, LUADN
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PARTEM: PC-DOS/MS-DOS
DEFAIL OF PARTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              Sequence 142, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 1313 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridge
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gesner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE:
US-07-757-022B-142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches 5
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525 STAPITPKKLIPITPEKLAPITPEKPAPITPESLAPITPESPAPITPESPAPTTPKAAAP 584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTPEVTPLRLELOKLPGLASTTLSTPNPDTQASASP----DPRPLREEEEARLLPRTHLQ 127
128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                 584 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTKEPAPTTPKKPAP 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.4%; Pred. No. 3.7e-05;
Matches 50; Conservative 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Clark, Stephen C.
APPLICANT: Hewick, Rotherine
APPLICANT: Hewick, Rodney M.
ITILE OF INVENTION: Megakaryocyte Stimulating Factors
INMER OF SEQUENCES: 143
CORRESPONDENCE ADDRES:
ADDRESSEE Genetics Institute, Inc.
STRET: 87 Cambridge
STRET: Amasachusetts
COUNTRY: U.S.A.
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SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/56,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
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591 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 646
                                                                    RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      531 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕЕГАРТТРЕЕРТРЕЕРАРТТРКАААР 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AELHQHGCWTVTEPAALT---PGNATPPRIQEVTPLLLELQKLPELVHATLSTPNP 180
                                                585 NTPKEPAPITPKEPAPITPKEPAPITPKETAPITPKGTAPTILKEPAPITPKKPAP 640
    128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
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                                                                                                                                                                                                                                                                                                                   Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.5%; Score 144; DB 4; 28.4%; Pred. No. 3.7e-05;
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RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
RRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                 B: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                       Sequence 46, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Glark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte St
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 44
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Cambridge
STATE: Massachusetts
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                         US-07-757-022B-46
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471 TTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPK 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
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Pred. No. 3.7e-05;
                                                                                                                                                                                                                                                    Megakaryocyte Stimulating Factors
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APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
PRIOR APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: US 07/457,196
FILING DATE: US 07/457,196
FILING DATE: US 07/457,196
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                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5190
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                       Sequence 60, Application US/07757022B
                                                                                                                APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: CBerr, Luann
REGISTATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 60: SEQUENCE CHARACTERISTICS:
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AMINO ACID
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Matches 50; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 02140
                                                        Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-757-022B-60
US-07-757-022B-60
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US 07/390,901
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08-AUG-1989
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                   FILING DATE: 08-AUG-1989 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.4%
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                          US-07-757-022B-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-757-022B-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471 ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТККРАРТТРКЕРАРТТРК 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 RIPEVIPLRIELOKI.PGLASITILSTPNPDIOASASP----DPRPLREEEEARLI.PRTHLQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      591 NTPKEPAPTIPKÉPAPTIPKEPAPTIPKETAPTIPKGTAPTILKÉPAPTIPKKPAP 646
                                                                                                 GENERAL INFORMATION:
APPLICANT: Origene Technologies, Inc
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
TITLE OF INVENTION: Regulated Angiogenesis Genes and Polypeptides
FILE REFERENCATION NUMBER: US/10/164,595
CURRENT APPLICATION NUMBER: US/10/164,595
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58
LENGTH: 1320
                                                                                                                                                                                                                                                                                                                                                                                                                             14.5%; Score 144; DB 4; Length 1320; 28.4%; Pred. No. 3.7e-05; Live 11; Mismatches 97; Indels 1
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APPLICANT Gesner, Thomas G.
APPLICANT Clark, Stephen C.
APPLICANT Turner, Ratherine
APPLICANT Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48, Application US/07757022B
Patent No. 6433142
                                                           Sequence 58, Application US/10164595
Patent No. 6657054
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match | 14.5%
Best Local Similarity 28.4%
Matches 50; Conservative
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Massachusetts
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                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U.S.A.
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US-07-757-022B-48
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STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                  US-10-164-595-58
                                      US-10-164-595-58
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72 RIPEVIPLREELQKLPGLASTILSIPNPDIQASASP----DPRPLREEEEARLLPRIHLQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  625 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 680
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 144; DB 4; Length 1354;
28.4%; Pred. No. 3.9e-05;
tive 11; Mismatches 97; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Megakaryocyte Stimulating Factors
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SASPDPRPLKEEERAPILPRTHLQAEPHQHGCWTVTEPAAMT-
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CURRENT APPLICATION DATA:
SELICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATE: 08-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,194
FILING PAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
APPLICATION NUMBER: US 07/200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 40, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Ratherine
APPLICANT: Turner, Ratherine
ITLE OF INVENTION: Megakaryocyte St
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
NAME: CBETT, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION:
TELEPHONE: (617)876-1170
                                                                                                TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 1354 amino acids
TYPE: AMINO ACID
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72 RIPEVIPLRIELQKLPGLASTILSTPNPDIQASASP----DPRPLREEEEARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  572 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕБІАРТТРЕБРТРТТРЕВРАРТТРКАААР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   632 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТСКЕРАРТТРККРАР 687
                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Gaps
                                                                                                                                                                                                                                                                                                                                                                              ch 14.5%; Score 144; DB 4; Length 1361; 1 Similarity 28.4%; Pred. No. 3.9e-05; 50; Conservative 11; Mismatches 97; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 SASPDPRPLKEEEEAPLLPRTHLQAEPHOHGCWTVTEPAAMT----
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 29-DEC-1989
ATTORNEY/AGENT INFORMATION:
NAME: CSETT, LUMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Genetics Institute, Inc.
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
TITLE OF INVENTION: Megakaryocyte St.
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                         GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               NAME: CRETK, LUADH
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI S:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 amino acids
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-07-757-0228-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                   TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 50; Conserv
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72 RTPEVTPLRLELQKLPGLASTTLSTPNPDTQASASP----DPRPLREEEEARLLPRTHLQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 634 МТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТІКЕРАРТТРККРАР 689
                                                                                                                                                                                                                                                                                                                                                  Gaps
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14.5%; Score 144; DB 4; Length 1363;
Best Local Similarity 28.4%; Pred. No. 3.9e-05;
Matches 50; Conservative 11; Mismatches 97; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                            23 SASPDPRPLKEEERAPLLPRTHLQAEPHQHGCWTVTEPAAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: February 19, 2005, 00:00:40
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMUNILOTION INCORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-1170
TELEFAX: (617)876-1170
TELEFAX: (617)876-1170
TELEFAX: (617)876-1170
TELEFAX: (617)876-1170
TELEFAX: (617)876-1170
                                                                                                                      LANCIH: 1363 amino acide
TYPE: AMINO ACID
TOPOLOGY: line
                                                                                                                                                                                                                                , MOLECULE TYPE: protein US-07-757-0228-52
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February 18, 2005, 23:59:14; Search time 130 Seconds (without alignments) 470.724 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1380268 seqs, 327241040 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      US-10-030-225-2_COPY_27_213
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 94, Appl	Sequence 403, App	Sequence 33474, A	Sequence 14, Appl		74,	Sequence 58, Appl	104,	44,	42,	142,	20,	Sequence 46, Appl
ID	US-09-939-853A-94	US-10-074-978A-403	US-09-864-761-33474	US-10-124-557-14	US-10-124-557-84	US-10-124-557-74	US-10-124-557-58	US-10-124-557-104	US-10-124-557-44	US-10-124-557-42	US-10-124-557-142	US-10-124-557-50	US-10-124-557-46
DB	11	15	6	13	13	13	13	13	13	13	13	13	13
% Query Match Length DB	658	538	81	941	1022	1038	1049	1140	1270	1311	1313	1314	1320
% Query Match	93.8	88.3	43.2	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5	14.5
Score	933.5	879	430	144	144	144	144	144	144	144	144	144	144
Result No.	-	7	m	4	S	9	7	æ	0	10	11	12	13

1404 1404 1404
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466
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345
537
19723 1518
582
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244
244
329
726
803
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881
487
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ALIGNMENTS

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Sequence 94, Application US/09939853A

; Sequence 94, Application US/09939853A
; Publication No. US20040039163A1
; GENERAL INFORMATION:
; TITLE OF INVENTION:
; PRIOR APPLICATION NUMBER: US/09/939,853A
; CURRENT FILING DATE: 2001-08-27
; PRIOR APPLICATION NUMBER: 60/229,191
; PRIOR APPLICATION NUMBER: 60/267,300
; PRIOR PILING DATE: 2001-02-08
; PRIOR PILING DATE: 2001-02-06
; PRIOR PILING DATE: 2001-02-06
; PRIOR PILING DATE: 2001-03-20
; PRIOR PILING DATE: 2001-03-20
; RIGHT APPLICATION NUMBER: 60/277,337
; PRIOR PILING DATE: 2001-03-20
; RIGHT APPLICATION NUMBER: 60/277,337
; PRIOR PILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: PATENTIN VET: 2.1
; SEQ ID NOS: 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VSASPDPRPLKE 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 67.5'
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-09-939-853A-94
JS-09-939-853A-94
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Gaps

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Indels

Length 538;

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 ELOKLPGLASTTLSTPNPDTQASASPDPRPLREEEFARLLPRTHLQAELHQHGCWTVTEP 141
                                                                                                                                                                                                                                                                                                                                                                                                             15 VSASPDPRFLKEBEBEAPLLPRTHLQABPHQHGCWTVTBPAAMTPGNATPPRTPEVTPLRL 74
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PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: 60/268,646
PRIOR PILING DATE: 2001-02-14
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 547
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 403
LENGTH: 538
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 AALTPGNATPPRIQEVTPLLIELQKLPELVHATLSTPNPDNQVTIK 180
                                                                                                                                                                                                                                                                                DB 15;
                                                                                                                                                                                                                                                                           Score 879; DB 15;
Pred. No. 4.1e-60;
1; Mismatches 1
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PRIOR PELIANG DATE: 2000-02-04
PRIOR PELING DATE: 2000-02-04
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-36
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-00-03
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APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
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Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                  88.3%;
98.8%;
                                                                                                                                                                                                                                                                                  Query Match 88.3
Best Local Similarity 98.8
Matches 164; Conservative
                                                                                                                                                                                                                , ORGANISM: Homo sapiens
US-10-074-978A-403
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                                                                                             147 EEBAPLLPRIHLQAEPHQHGCWIVTEPAAMTPGNATPPRITPEVIPLRLELQKLPGLANIT 206
                                                                                                                                                                           LSTPNPDTQASASPDPRPLREEEBARLLPRTHLQAELHQHGCWTVTEPAALTPGNATPPR 153
       ERGAGAGRKLPDTGRCPVTEGSTVQLIAPWNAADVHSHGDKDSQTCIRVSASPDPRPLKE 146
                                                        EEEAPLLPRIHLQAEPHQHGCWIVTEPAAMIPGNITPPRIPEVIPLRLELQKLPGLASTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Smithson, Glennda
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
TIER REPRENCE: 21402-269
CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT FILING DATE: 2003-01-07
                                                                                                                                                                                                                                             TOEVTPLILELOKLPELVHATLSTPNPDNQVTIK 187
                                                                                                                                                                                                                                                                        Pena, Carol E A
Shimkers, Richard A
Taupier Jr, Raymond J
Moore, No. US20040010119Allle
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PRIOR FILING DATE: 2001-07
PRIOR FILING DATE: 2001-02-12
PRIOR FILING DATE: 2001-10-31
PRIOR FILING DATE: 2001-10-31
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 403, Application US/10074978A Publication No. US20040010119A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-10-31
APPLICATION WINBER: 60/312,284
FILING DATE: 2001-08-14
APPLICATION NUMBER: 60/268,496
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APPLICATION NUMBER: 60/276,703
FILING DATE: 2001-03-16
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APPLICATION NUMBER: 60/280,899
FILING DATE: 2001-04-02
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APPLICATION NUMBER: 60/310,797
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Guo, Xiaojia (Sasha)
Fernandes, Elma
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Casman, Stacie
Boldog, Ferenc
Patturajan, Meera
Blalock, Angela
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Malyankar, Uriel M
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Millet, Isabelle
Peyman, John
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Mezes, Peter S
Ellerman, Karen
Heyes, Melvin P
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Gunther, Erik
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Kekuda, Ramesh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrman, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 VSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N: EXPRESSED IN BT474, SIGNAL = 0.85

N: EXPRESSED IN BONE MARROW, SIGNAL = 0.92

N: EXPRESSED IN HELLOO, SIGNAL = 0.92

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75

N: EXPRESSED IN LUNG, SIGNAL = 0.92

N: EXPRESSED IN LUNG, SIGNAL = 0.96

N: EXPRESSED IN BADUT LIVER, SIGNAL = 0.96

N: EXPRESSED IN HELA, SIGNAL = 1.4

N: EXPRESSED IN HEART, SIGNAL = 1.4

N: EXPRESSED IN HEART, SIGNAL = 1.4

N: EXPRESSED IN HEART, SIGNAL = 1.4

N: EXTHUMAN HIT: BE281519.1, EVALUE 1.30e+00

N: STI HUMAN HIT: BE281519.1, EVALUE 2.00e-31

N: SWISSPROT HIT: Q02817, EVALUE 5.30e+00
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Radney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 81;
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
NUMBER: OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 33474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLACENTA, SIGNAL =
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Pred. No. 3.4e-26;
1; Mismatches 1;
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STREET: 87 CambridgePark Drive
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CLASSIFICATION: «Unknown»
APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/124,557
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELOKLPGLASTILSTPNPDTQ 102
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COUNTRY: U.S.A.
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97.5%;
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COMPUTER READABLE FORM:
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1es 79; Conservative
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356 TTTKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTPKEPAPTTKKPAPTAPKEPAPTTPK 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРІТРЕЕLАРТТРЕЕРТРТРЕЕРАРТТРКАААР 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.5%; Score 144; DB 13; Length 941; 28.4%; Pred. No. 0.0083; tive 11; Mismatches 97; Indels 10
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RTLING DATE: 16-Apr-2002
CLASSIFICATION: <university control Numbers: us/10/124,557
FTLING DATE: 16-Apr-2002
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         TELEFAX: (617)876-581
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acids
; TYPE: amino acids
; POPOLOCY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-124-557-14
                       FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/546,114
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APPLICATION NUMBER: US 07/546,114
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APPLICATION NUMBER: US 07/457,196
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                                                                                                                                                                                          NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION
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COUNTRY: U.S.A.
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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Best Local Similarity
Matches 50; Conserva
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COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 ВТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕВІАРТТРЕЕРТРЕВРАРТТРКАААР 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- PGNTTPP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     557 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKBPAPTTPKKPAP 612
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                  Length 1022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Genner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORREGPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                             97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
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                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 144; DB 13; 28.4%; Pred. No. 0.0091; tive 11; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION UNMER: US 07/643,502
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
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MEDIUM TYPE: FLORDBY disk
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACEDIAIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                              NAME: Cserr, Luann
REGISTRATION UNMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 84: US-10-124-557-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 74, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                             TELEPHONE: (617)876-1170
TELEPRA: (617)876-5891
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                LENGTH: 1022 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.49
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US-10-124-557-74
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Matches
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RIPEVTPLRIELQKLPGLASTILSTPNPDIQASASP----DPRPLREEEEARLLPRIHLQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                   Length 1038;
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 28.4%; Pred. No. 0.0093;
Matches 50; Conservative 11; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 74:
US-10-124-557-74
NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51:8
TELECOMMUNICATION INPORMATION:
TELEPHONE: (617)876-1170
TELEPAK: (617)876-1170
INFORMATION FOR SEQ ID NO: 74:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 58, Application US/10124557; Publication No. US20020137894A1
                                                                                                                                                                                                   LENGTH: 1038 amino acids
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SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   524 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕЕЛАРТТРЕЕРТРТТРЕЕРАРТТРКАААР 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    584 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТСКЕРАРТТРККРАР 639
                                                                                                                                                                                                                                                                      14.5%; Score 144; DB 13; Length 1049; 28.4%; Pred. No. 0.0094; ive 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                  23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTBPAAMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNT APPLICATION DATA:
SPELICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIPICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             7 TOPOLOGY: linear
7 MOLECULE TYPE: protein
7 SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-124-557-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 104, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER:
                                                        TELEFAX: (617)876-5851
WANTION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 1049 amino acids
                   TELECOMMUNICATION INFORMATION
                                         (617)876 - 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                               50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Cambridge
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                                         TELEPHONE:
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-124-557-104
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555 ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТТККРАРТАРКЕРАРТТРК 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 RIPEVTPLRLELQKLPGLASTILSTPNPDTQASASP----DPRPLREEEBARLLPRTHLQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕБІАРТТРЕЕРТРТТРЕЕРАРТТРКАААР 674
                                                                                                                                                                                                                                                                                                                                                                             7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     675 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 730
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                        Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 44, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             23 SASPDPRPLKEEERAPLLPRTHLQAEPHOHGCWTVTEPAAMT
                                                                                                                                                                                                                                                                  Query Match
14.5%; Score 144; DB 13;
Best Local Similarity 28.4%; Pred. No. 0.01;
Matches 50; Conservative 11; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/643,502
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                                                                                                                                               MOLECTLE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-124-557-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07 FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
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                                                                           LENGTH: 1140 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-DEC-1989
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FILING DATE: 08-AUG-1989
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TELEFAX: (617)876-56
INFORMATION FOR SEQ ID NO: 104
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02140
COMPUTER READABLE FORM:
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                                                                                                          TYPE: amino acid
                                                                                                                                    TOPOLOGY: linear
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RESULT 11
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                                                                                                                                                                                                                                                                            481 ЕТАРТТРККІТРТТРЕКІАРТТРЕКРАРТТРЕЕГАРТТРЕЕРТТРКАЛАР 540
                                                                                                                                                                                                                                                                                                                                            72 RTPEVTPLRLELQKLPGLASTTLSTPNPDTQASASP----DPRPLREEEEARLLPRTHLQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                   128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 596
                                                                                                                                                                                                        18; Gaps
                                                                                                                                                         Query Match 14.5%; Score 144; DB 13; Length 1270; Best Local Similarity 28.4%; Pred. No. 0.012; Matches 50; Conservative 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodrey M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-App-2002
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNW-1990
APPLICATION NUMBER: US 07/457,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (617)876-1170
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LENGTH: 1270 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 42, Application US/10124557
Publication No. US20020137894A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (617)876-5851
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
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US-10-124-557-42
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                                                                                                                                                                                                                                                                                  72 RIPEVIPLRIBLOKLPGLASTILSTPNPDIOASASP----DPRPLREEBEARLLPRIHLQ 127
                                                                                                                                                                                                                                                                                                                                                                           128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                         582 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТГКЕРАРТТРККРАР 637
                                                                                                                                              Gaps
                                                                                                                                              18;
                                                                                           14.5%; Score 144; DB 13; Length 1311; 28.4%; Pred. No. 0.012; Live 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 142, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
MDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Pc-ease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                              23 SASPDPRPLKEEERAPLLPRTHLQAEPHOHGCWTVTEPAAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 9-DEC-1989
FILING DATE: 08-AUG-1989
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FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
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***TOPOLOGY: linear
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***MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-124-557-142
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) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-124-557-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
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REGISTRATION NUMBER: 31,822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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SEQUENCE CHARACTERISTICS:
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                                                                             Query Match
Best Local Similarity 28.*.,
Best Local So, Conservative
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Gaps

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72 RIPEVTPLREELQKLPGLASTTLSTPNPDTQASASP----DPRPLREEEBARLLPRTHLQ 127
                                                                                                                                                                                  525 ЕТАРТТРККЦТРТТРЕКЦАРТТРЕКРАРТТРЕЕLАРТТРЕЕРТРТРЕЕРАРТТРКАААР 584
                                                                                                                                                                                                                                128 AELHOHGCWTVTEPAALT----PGNATPPRTOEVTPLLLELOKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                           585 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТСКЕРАРТТРККРАР 640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.5%; Score 144; DB 13; Length 1320; 28.4%; Pred. No. 0.012; Live 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
INVENTION: Megakaryocyte Stimulating Factors
  97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
                                               23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
    Mismatches
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FILING DATE: 18-JAN-1991
PILING DATE: 29-JUN-1990
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457;196
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APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
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SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-124-557-46
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 46, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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    11;
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COUNTRY: U.S.A.
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NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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    Conservative
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US-10-124-557-46
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  Matches
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                                                                                                                                                                                                        72 RTPEVTPLRLELQKLPGLASTTLSTPNPDTQASASP----DPRPLREEEEARLLPRTHLQ 127
                                                                                                                                                                                                                                  524 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPTPTTPKAAAP 583
                                                                                                                                                                                                                                                                                                128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
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                                                                       Gaps
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                          Length 1313;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                     ; Score 144; DB 13; Length 1; Pred. No. 0.012; 11; Mismatches 97; Indels
                                                                                                             23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
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28.4%; Pred. No. 0.012;
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
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FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-124-557-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50, Application US/10124557 Publication No. US20020137894A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Turner, Katherine
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SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: Massachusetts
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                       14.5%;
28.4%;
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COMPUTER READABLE FORM:
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                                                                  50; Conservative
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Best Local Similarity
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US-10-124-557-50
                   Query Match
Best Local Si
Matches 50;
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72 RIPEVIPLRIELQKI.PGLASITLSIPNPDIQASASP----DPRPLREEEEARLLPRIHLQ 127
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-10-124-557-48
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
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US-10-124-557-48
Sequence 48, Application US/101245>,
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
APPLICANT: Turner, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617)876-1170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
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Best Local Similarity
Matches 50; Conserv
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                                                                                                                                            128 AELHQHGCWIVIEPAALI---PGNAIPPRIQEVIPLLIELQKLPELVHAILSTPNP 180
                                                                                                                                                                                   591 NTPKEPAPTTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKKPAP 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.5%; Score 144; DB 13; Length 1320; larity 28.4%; Pred. No. 0.012; Conservative 11; Mismatches 97; Indels 18
                                                                                                                                                                                                                                                                                                                                                                             Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SNT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
CLASSIFICATION: <u >- CUNKNOWN></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 60: US-10-124-557-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                    Sequence 60, Application US/10124557
Publication No. US20020137894A1
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                  Clark, Stephen C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
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Best Local Similarity
Matches 50; Conserv
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US-10-124-557-60
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505 TTTKEPAPTTPKEPAPTTPKKPAPTTPKEPAPTTPKEPAPTTTKKPAPTAPKEPAPTTPK 564
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531 ETAPTTPKKLTPTTPEKLAPTTPEKPAPTTPEELAPTTPEEPTPTTPEEPAPTTPKAAAP
                                                             128 AELHQHGCWTVTEPAALT---PGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                       591 ИТРКЕРАРТТРКЕРАРТТРКЕРАРТТРКЕТАРТТРКСТАРТТСКЕРАРТТРККРАР 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1354;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UNN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
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Search completed: February 19, 2005, 00:11:41 Job time: 134 secs

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February 18, 2005, 23:50:22 ; Search time 39 Seconds (without alignments) 461.347 Million cell updates/sec
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995
1 LPVKKPRLRGPRPGSLTRLA.....PELVHATLSTPNPDNQVTIK 187
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             283416 seqs, 96216763 residues
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                            Title:
Perfect score:
                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                          Run on:
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283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	h DB ID . Description	0 2 D89756 protein T23E7.2b [2 A37232	2 T51023	2 E84682 hypothetical	2 I51920 mucin - rhesu	2 S27721 hypothet	2 T30826	2 F59433	2 T19050	2 A43932	1 QQBE8	2 E70546	2 T21700 hypothetical	2 A45690 transactivato	2 C87437	2 S47143	2 A33532	2 A35363	2 T03454	2 \$35332	2 A48018	2 T42730	2 S13383	2 T52340	2 T12526	1 S68235 myosin-light-	2 T15336	
	Length	880	294	2649	653	216	291	2187	803	1186	3020	3149	548	846	530	794	524	167	705	5262	283	377	3942	283	306	915	1906	798	
de	Query	12.4	12.3	11.8	11.8	11.7	11.7	11.6	11.5	11.5	11.4	11.3	11.2	11.2	11.0	11.0	11.0	10.9	10.9	10.9	10.9	10.9	10.7	10.7	10.7	10.7	10.7	10.6	
	Score	123	122	117.5	117:	116.5	116	115.5	114.5	114	113	112	111.5	111	109.5	109.5	109	108.5	108.5	108.5	108	108	106.5	106	106	106	106	105.5	
	Result No.	1	7	m	4	Ŋ	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	

RESULT 2

mucin, tracheal (AMN-22) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
C;Accession A37232
R;Gerard, C; Eddy Jr., R.L.; Shows, T.B.
J. Clin. Invest. 86, 1921-1927, 1990
J. Clin. Invest. 86, 1921-1927, 1990
J. R;Gerard Cr. Februard Cr.

hydroxyproline-ric	gag-like protein -	US4 protein - huma	elastic titin - hu	probable serine/th	hypothetical prote	coagulation factor	mucin JER57 - huma	zinc metalloprotei	alpha-A-crystallin	translocation prot	translation initia	voltage-dependent	zinc finger protei	hypothetical prote	OP protein - Kenne
28264	7,000	43674	I38346	T05264	F75518	KFBOS	835049	H95076	I49477	383434	144453	rc5280	522293	r04455	JQ0532
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7	613 2 T	~	~	674 2	839 2	2211 1	610 2	1881 2	2688 2	~	~	N	~	~	753 2
303 2	7	699 2	7962 2			•		•	•••	369 2	1396 2	2206 2	670 2	731 2	
10.6 303 2	613 2	10.6 699 2	10.6 7962 2	10.5	10.5	10.5	10.5	10.4	10.4	10.4 369 2	10.4 1396 2	10.4 2206 2	10.3 670 2	10.3 731 2	10.3

ALIGNMENTS

RESULT 1 D89756 protein T23E7.2b C;Species: Caenor. C;Date: 10-May-20 C;Accession: D897 R;anonymous, The Science 282, 2012 A;Tile: Genome 8 A;Reference numbe A;Note: see websi A;Note: published A;Note: published A;Note: published A;Note: published A;Note: published A;Note: published A;Note: published A;Note: published A;Note: published A;Cossi published A;Cossi published A;Cossi published A;Cossi published A;Cossi published A;Cossi published A;Cossi published A;Cossi published A;Cossi published A;Gossi publishe	RESULT 1 D89756 Cypecies: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: D89756 C;Accession: D89756 C;Accession: D89756 C;Accession: D89756 A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Title: Genome sequence of the nematode C. elegans: and www sanger.ac.uk/Projects/C_ele A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: D89756 A;Accession: D89756 A;Accession: DNA A;Residues: 1-880 <sto> A;Residues: USB0 <sto> A;Cossa-references: UNIPROT:017338; GB:chr_X; PIDN:AAB71258.1; PID:g2435547; GSPDB:GN000 C;Gene: T23E7.2b A;Map position: X</sto></sto>
Query Match Best Local Matches 4	Query Match 12.4%; Score 123; DB 2; Length 880; Best Local Similarity 26.9%; Pred. No. 0.21; Matches 45; Conservative 14; Mismatches 62; Indels 46; Gaps 7;
% 8	35 EEAPLLPRTHLOAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRLELQKLPGLAS 91
& 92	92TILSTPNPDTQASASPDPRPLREEEBARLLPRTHLQAELHQHGCWTVTEPA 142
 Qa	143 ALTPGNATPPRTQEVTPLLLE-LQKLPELVHATLSTPNP 180

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84682
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-653 <STO>
A;Cross-references: UNIPROT:Q9SL31; GB:AE002093; NID:g4803957; PIDN:AAD29829.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mucin - rhesus macaque (fragment)
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 151920
R;An, G:; Mu, R.
Am. J. Respir. Cell Mol. Biol. 10, 546-551, 1994
A;Title: Expression of MUC2 gene is down-regulated by vitamin A at the transcriptional 1
A;Reference number: 151920; MUD:942322; PMID:8179918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q28501; EMBL:U00483; NID:g437054; PIDN:AAA20963.1; PID:g4370
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLREEE------EARLLPRTHLQAB---LHQHGCWT-VTEPAALTPG------NAT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 PIPOKALVOANTDINSTALPRPLVTÄEAPPLHÖSSCKAPOPKPISQOPAVOSKTDIINST 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 PTPITI-TTTTTTTTPTPTSTQTPTP-TPIT------SNTTAMTPTPTPT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 PPRTPEVTPENTELGKLPGLASTTLSTPNPDTQASASPDPRPLREEEEARLLPRTHLQAE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 TEPAAMTPGNTTPPRTPEVTPLRLELOKLPGLASTTLSTPNPDTOA-----SASPDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 PRIRGPRPGSLTRLAEVSASPDPRPLKEEE-----EAPLLPRTHLQAEPHQHGCWTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 PRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNT-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PPRIQEVIPLLLELQKLPELVHATL------SIPNPDNQVTIK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 ALPRPSUTTEARPLHQPRSKTPQPKPVSQPPAKQSNTEINSTPHPRPSVTSK 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 STQTPTVTPI ------TTTTTTATPTPTPTSTQTPTPTPTPTFIT-----
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                                                                                                                                                                                                                                                                                                                                                                                     Length 653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 82; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54:
                                                                                                                                                                                                                                                                                                                                                                                  11.8%; Score 117; DB 2; 24.6%; Pred. No. 0.4; ive 23; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-216 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.7%; Score 116.5; DB
25.7%; Pred. No. 0.13;
tive 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Conservative
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Matches 44: Conser
                                                                                                                                                                                                                                                                                      A.Gene: At2g28240
A.Map position: 2
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Cispecies: 1-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
Cispecies: 1-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
Cispecies: 151023
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hypothetical protein At2g28240 [imported] - Arabidopsis thaliana
hypothetical protein At2g28240 [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84682
R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
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                                                              Length 294;
                                                                                                                                                                                       11 PRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTV-
                                                                                                                            Indels
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                                                       Query Match 12.3%; Score 122; DB 2; Best Local Similarity 23.6%; Pred. No. 0.075; Matches 46; Conservative 16; Mismatches 91;
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   UNIPROT: Q99322; GB: M57417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 KLPELVHATLSTPNP 180
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Best Local Similarity 26.0%
Matches 54; Conservative
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A;Introns: 1619/3; 2584/1
A; Cross-references:
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Rhodar protein [imported] - human C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Species: P59433; G59433 R.Stichnau, N.; Aspenstrom, P. J. Biol. Chem. 276, 35060-35070, 2001 A.Fitle: Rich, a rho gtpase-activating protein domain-containing protein involved in signature number: F59433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA_
A;Residues: 1-803 <RIC>
A;Crose-references: UNIPROT:Q96KS3; GB:CAC37948; PID:g13940243; PIDN:CAC37948.1
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                                                                                                                                                                                                       1078 SPKTAGPKETPPGGVTAVPPEISLPPKETPQNATPNESLAASSQKRSPKTSVPKETPPGG 1137
                                                                                                                                                                                                                                                                                                                                                                   1018 TAAPKESSATSSSKRAPKTAVSKEIPSKGVTAVPLEISLPLKETSKSATPGEKSASSPKR 1077
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C;Accession: T19050
R;Matthews, P.
                     2 PVKKPR---LRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVT
                                                             2 PVKKPRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLL---PRT----HLQAEPHQHGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: CAC37948; PID: 913940243; PIDN: CAC37948.1
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                                                                                                                                                           59 EPAAMTPGNTTPPRTPEVTPLRLELQKLPGLASTTLSTPNPD--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, June 1995
A;Reference number: 219066
A;Accesion: T19050
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 VTPLLLELQKLPELVHATL---STPNPDNQVTI 186
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                                                                                                                                                                                                                                                                                              106 SPDPRPLREEEBARLLPRTHLQAELHQHGCWTV-
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Best Local Similarity 27.5%
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submitted to Genbank, April
A;Reference number: G59433
A;Accession: G59433
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C;Date: 17-Apr-1993 #sequence revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: S33615; S75613; $\overline{\text{S27721}} \text{R}_i Malakhov, Mr. P; Wadad, H:;Los, D.A.; Sakamoto, T:; Murata, N.
Plant Mol. Biol. 21, 913-918, 1993
A;Title: Structure of a cyanobacterial gene encoding the 50S ribosomal protein L9.
A;Recence number: S33614; MUID: 93222488; PMID: 8467083
A;Accession: S33618
A;Accession: S33618
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-291 AMA2>
A;Cross-references: UNIPROT: P42350; GB:D10716; NID: g217098; PIDN: BAA38818.1; PID: d100203
A;Cross-references: UNIPROT: P42350; GB:D10716; NID: g217098; PIDN: BAA38818.1; PID: d100203
A;Cross-references: UNIPROT: P42350; GB:D10716; NID: g217098; PIDN: BAA38818.1; PID: d100203
A;Cross-references: UNIPROT: P42350; GB:D10716; NID: g217098; PIDN: BAA38818.1; PID: d100203
A;Cross-references: UNIPROT: P42350; GB:D10716; NID: g10311 Library, April 1992
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
B;Accession: S75613
A;Status: preliminary
A;Accession: S75613
A;Status: preliminary
A;Accession: S75613
A;Cross-references: EMBL: D90912; GB:AB001339; NID: g1653228; PIDN: BAA18174.1; PID: d101890
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nascent polypeptide-associated complex alpha chain, muscle splice form gp220 - mouse nakeent polypeptide-associated complex alpha-NAC protein C; Species: Mus musculus (house mouse)
C; Date: 22-Oct.1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C; Date: 22-Oct.1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C; Accession: T30826
R; Yotov, W.V.; St-Arnaud, R. Genes Dev. 10, 1763-1772, 1996
A; Title: Differential splicing-in of a proline-rich exon converts alphaNAC into a muscle A; Reference number: 220889; MulD:96312450; PMID:8698236
A; Accession: T30826
A; Accession: T30826
A; Accession: T30826
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A;Introns: 24/1; 1996/1; 2024/3; 2050/3; 2099/3; 2142/3; 2183/3
A;Note: differential splicing converts alphaNAC into a tissue-specific DNA-binding
C;Keywords: alternative splicing; DNA binding; transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPEVTPLRLELQKLP----GLASTTLSTPNPDTQASASPDPRPLREEEEARLLPRTHLQA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQ-----KLPELVHATLSTPNPDN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.7%; Score 116; DB 2; Length 291; Best Local Similarity 26.8%; Pred. No. 0.2; Matches 49; Conservative 21; Mismatches 61; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.6%; Score 115.5; DB 2; Length 2 ilarity 20.5%; Pred. No. 1.9; Conservative 32; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVT 185
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J. Biol. Chem. 264, 6480-6487, 1989
A;Title: Molecular cloning of human intestinal mucin cDNAs. Sequence analysis and eviden.
A;Reference number: A33532; MUID:89197956; PMID:2703501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rixu, G.; Huan, L.; Khatri, I.; Sajjan, U.S.; McCool, D.; Wang, D.; Jones, C.; Forstner, Blochem. Blophys. Res. Commun. 183, 281-828, 1992. A.; Forst Res. Commun. 11ke protein (MLP) is homologous with rat MLP in the C-t A;Reference number: PQ0328; MUID:92198477; PMID:1550588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P03186; EMBL:V01555; NID:g59074; PIDN:CAA24839.1; PID:g13348 R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B95-8 Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:120203; OMIM:158370
A;Map position: 11p15.5-11p15.5
C;Superfemily: von Willebrand factor; von Willebrand factor type A repeat homology; von C;Superfemily: vor Willebrand factor; tandem repeat
C;Keywords: gjycoprotein; intestine; tandem repeat
F;2766-2834/Domain: von Willebrand factor type C repeat homology <VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1583 TYTPSPPTITTTPPPTTTTPSPPTTTTPPPPTTTPS-PPTTTPITPPTSTTTLPPTTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1642 S---pppTTTTppppTTTpSppTTTpSppITTTTppppTTTpSSpITTTpSppTTTMTT 1698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1526 PITITITIPPPITITPSPPITITPITITPTSTTLAPTITPSSP---PITITAPPITITPSPPI 1582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 AELHQHGCWTVTEPAALTPGNAT-----PPRTQEVTP----LLLELQKLPELVHATLST 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 PGSLTRLAEVSASPDP---RPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPG--N
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                                                                                                                                                                  A;Wolecule type: mRNA
A;Residuse: 1916-2123 <UU4>
A;Cosderences: GB:M22405; NID:g188873; PIDN:AAA36334.1; PID:g188874
A;Experimental source: intestine
                                                                                                                                                                                                                                                                                                             R.Jany, B.H.; Gallup, M.W.; Yan, P.S.; Gum, J.R.; Kim, Y.S.; Basbaum, J. Clin. Invest. 87, 77-82, 1991
A.Title: Human bronchus and intestine express the same mucin gene.
A.Reference number: A61257; MUID:91086481; PMID:1985113
A.Accession: A61257
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C;Date: 25-Feb-1985 #sequence revision 25-Feb-1985 #text_change
C;Accession: G93065; A03747; S32993
R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
Mol. Biol. Med. 1, 21-45, 1983
A;Title: Sequence analysis of the 17,166 bp EcoRI fragment C of 1
A;Reference number: A93065; MUID:85035713; PMID:6092825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecule type: mRNA
Residues: 'T',1925-1948,'TTS',1952-1954 <JAN>
Experimental source: bronchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 2328-2342,'K', 2344-2354 <XUG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 238-2468 xUG>
Cross-references: GB:M85523
A;Experimental source: small intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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A;Residues: 1-3149 <BAN>
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hes 48; Conserv
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                                                                                                                               A; Accession: B33532
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Natherate names amoning Marca-1

C) Apecies: Homo eapiens (man)

C) Apecies: Homo eapiens (man)

C) Date: 10-Mar-1939 #sequence_revision 12-Apr-1936 #text_change 09-Jul-2004

C) Accession: A49963; A45106; E45106; A49932; B3532; A61257; P60328; P60329

R) Gum Jr., J.R.; Hicks, J.W.; Torbara, N.W.; Siddikt, B.; Kim, Y.S.

J. Biol. Chem. 269, 2440-2446, 1998

A) Teleiem Comman and A9963; MUID: 94132002; PMID: 9300571

A) Accession: A49963; MUID: 94132002; PMID: 9300571

A) Accession: A49963

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A) Accession: A45066; MUID: 93016075; PMID: 1400449

A) Accession: A45106

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A) Accession: A45106

A) Accession: A409131; MUID: 9186395; PIDN: AA59163.1; PID: 9186396

A) Accession: A45106

A) Accession: A409132; Accession: A4001338

A) Accession: A45106

A) Accession: A409132; Accession: A4001338

A) Accession: A4091339

A) Accession: A409139

A) Accession: A409139

A) Accession: A409139

A) Accession: A400139

A) Acc
A;Molecule type: DNA
A;Residues: 1-1186 <WIL>
A;Residues: U-1186 <WIL>
A;Cross-references: UNIPROT:Q17786; EMBL:Z49908; PIDN:CAA90094.1; GSPDB:GN00020; CESP:CG
A;Experimental source: clone C07E3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <TOR;
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A;Residues: 1343-1350,'L',1352-1411,'S','1413-1448,'P',1450-1503,'T',1505-1915 <TG
A;Cross-references: GB:M74027; NID:g188663; DDN:AAA59875.1; PID:g188864
A;Note: sequence inconsistent with the mucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:55749, NCBIP:55750)
R;Gum, J.R.; Byrd, J.C.; Hicks, J.W.; Toribara, N.W.; Lamport, D.T.A.; Kim, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 ASPDPRPLREEEEARLLPRIHLQAELHQHGCWT---VTEPAALIPGNAIPPRIQEVTPLL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VKKPRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               744 RNVVSPSRYTPP--PSVTMAAKLHLTPLQPEVPSTPLQHYISRSRASSVYNTPSVD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      798 -STSTRSLVSPSSVRMPPKLHL-TRLQQDVPWTPFKVSRPRS-TPIYSTPP.
                                                                                                                                                                                                                                                                                                                                                         Length 1186;
                                                                                                                                                                                                                                                                                                                                                                                                                                 71,
                                                                                                                                                                                                                                                                                                                                                         Query Match 11.5%; Score 114; DB 2; Best Local Similarity 27.3%; Pred. No. 1.2; Matches 54; Conservative 19; Mismatches 71;
                                                                                                                                                                                                                                                                              A; Introns: 36/3; 79/3; 1128/3; 1160/3
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                                                                                                                                                                                                      Gene: CESP:C07E3.3
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A, Map position: 2
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submitted to the EMBL Data Library, January 1997
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                                                                                                                                                                                                                  A; Map position: 1
A; Introns: 99/3; 213/3; 332/3; 525/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----DIQASASPDPRPLREE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.0%;
22.4%;
                                                                                                                                                                                                                                                                                                    Best Local Similarity 24.99
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 PNPDNQVTIK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 TPNPDNQVT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       730 APRTEVPMT 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                              A; Gene: CESP: F33E2.6
                                                                                      A; Molecule type: DNA
A; Residues: 1-846 < W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Molecule type: DNA
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C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Accession: E70546
R; Connor, R.; Parosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davise, R.; Devlin, K.; Feltwell, T.; Churcher, C.; Harris, D.; Gordon, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Natures 393, 537-544, 1998
A; Authors: Sqares, R.; Suleton, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Recence number: A70500; MUID: 98295987; PMID: 9634230
A; Recence number: A70500; MUID: 98295987; PMID: 9634230
A; Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-548 <COL>
A; Cross-references: UNIPROT: 006404; GB: Z95558; GB: AL123456; NID: 93261781; PIDN: CAB08989.
C; Genetics:
A; Genetics:
A; Genetics:
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                                                                                                                                                                                                                                                                                                                                                 507
                                                                                                                                                                                                                                                                                                                                                                                        GLASTT----LSTPNPDTQASASP----DPRPLREEEEARLLPRTHLQAELHQHGCWTV 138
                                                                                                                                                                                                                                                                                                                                                                                                                   360 PRPGTSPGVGGTPASPAP-----EAPAVPGVVPAPVPIPVPIIIPPFPGWOPGMPTIP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPAAMTP---GNTTPPRTPEVTPLRLELQKLPGLASTTLSTPNPDTQASASPDPRPLREE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
                        the B95-8 Epstein-Barr virus genome. 67; PMID:6087149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T21700
hypothetical protein F33E2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21700
R;Lennard, N.
                                                                                                                                                                                                                                             | | : | | | | | | PAPSTPPRASSGAAPQTPKRKKGLGKDSPHKKPTSGRRLPLSSTTDTEDDQLPRTHVPPH
                                                                                                                                                                                                                                                                                                                                        455 RPPSAARLPPPVIPIPHQ-----SPPASPTP-HPAPVSTIAPSVTPSPRLPLQIPIPLP
                                                                                                                                                                                                                  ----PLKE--EEEAPLLPRTHLQAE
                                                                                                                                                                                                                                                                                                      --PHQHGCWTVTEPAAMTPGNTTPPRT--PEVTPL-RLELQ---KLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 548;
                                                                                                                                Length 3149;
                                                                                                                                                                          79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 TEPAALTPGNATPPRIQEV-TPLLLELOKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAPSPLLPQQQPPPSAARAPSPLPPQQQPLPS----ATPAP 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84;
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                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.2%; Score 111.5; DE 26.6%; Pred. No. 0.82; tive 10; Mismatches
Nature 310, 207-211, 1984
A;Title: DNA sequence and expression of the B95-8
A;Reference number: A03794; WUID:84270667; PMID:6
A;Contents: annotation; protein coding region
C;Superfamily: human herpesvirus 4 BPLF1 protein
                                                                                                                              11.3%; Score 112; DB
25.6%; Pred. No. 5;
:ive 21; Mismatches
                                                                                                                                                                                                                  11 PRPGSLTRLAEVSASPDPR-------
                                                                                                                                                  Best Local Similarity 25.6
Matches 57; Conservative
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Matches 4
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A;Cross-references: UNIPROT:001699; EMBL:Z84574; PIDN:CAB06541.1; GSPDB:GN00019; CESP:F3
A;Experimental source: clone F33E2
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-530 <LIN>
A;Cross-references: UNIPROT:Q07701; GB:L11366; NID:g6690013; PIDN:AAA79034.1; PID:g30631
A;Note: sequence extracted from NCBI backbone (NCBIN:132361, NCBIP:132362)
C;Superfamily: hydroxyproline-rich glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: A45690
R,Ling, P.D.; Ryon, J.J.; Hayward, S.D.
J. Virol. 67, 2990-3003, 1993
A,Title: EBNA-2 of herpesvirus papio diverges significantly from the type A and type B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 TPGNTTPPRT-----PEVTPLRLELQKLPGLASTTLSTPNPDTQASASPDPRPLREEE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 EARLLPRTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EEARLLPRIHLQABLHQHGCWIVTE 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLPLPPLSTPPPPPAPSTPSPGIVRDRPTSPRPLGPVWWPPVPLPEHKLAGPDLLTPSFDP 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 PRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLL - - PRTHLQAEPHQHGCWTVTEPAAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624 EPPRTAPPRTEVSMTLPPETVPPNTEAPR----TEVPMTVP-PRTEPPKTEAPRTVPPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 VPRPRMTILRPLTPLRLIRPPRPTYNPLSSPNTPSPSPIPF---QHTPLPPRPPTASPPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 QHGC-----WIVTEPAAMTPGN--TTPPRTPEVTPLRLELQKLPGLAST----TLSTPNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 VKKPR------LRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPH
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                                                                                                                                                                                                                                                                                                                                    Length 846;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transactivator EBNA-2 - baboon lymphotropic virus
C;Species: baboon lymphotropic virus, herpesvirus papio HVP
C;bate: 21-5ep-1993 #sequence_revision 25-Apr-1997 #text_ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: A45690; MUID:93267743; PMID:8388484
                                                                                                                                                                                                                                                                                                                                                                                           92;
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                                                                                                                                                                                                                                                                                                                                    11.2%; Score 111; DB 2; 24.9%; Pred. No. 1.4;
A;Reference number: 219461
A;Accession: T21700
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109.5; [
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                        20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25; Mismatches
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379 PIPEEETVRK 388

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Denicillin-binding protein, 1A family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: C87437
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession: C87437
A;Accession: C87437
A;Accession: C87437
A;Accession: C87437
A;Accession: C87437
A;Residues: 1-794 <STO>
A;Residues: 1-794 <STO>
A;Conetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PVKKPRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.0%; Score 109.5; DB 2; Length 794;
Best Local Similarity 27.1%; Pred. No. 1.7;
Matches 49; Conservative 18; Mismatches 79; Indels 35; Gaps
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62 AMTPGNTTPPRTPEVTPLRLELQKLPGLASTTLSTPNPDTQ-ASASPDPRPLREEEEARL 120

6 6 6 6

68 AQTPTTSTAATDDADADL---FEPLP----SPEPDAEPVSVEADPAETLEADAA-- 114

Search completed: February 18, 2005, 23:59:49 Job time : 42 secs

181 D 181 | | 161 D 161 arabidopsis arabidopsis macaca mula yarrowia li

synechocyst bacillus ce triticum ae

mus musculu mus musculu homo sapien caenorhabdi mus musculu streptomyce

Q98131 Q84jk0 Q6c8501 Q6c8501 Q6c8501 Q74p34 Q981r6 Q981r6 Q90515 Q90515 Q90515 Q80462

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result

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121 LPRTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C TISSUE-Placenta;
C TISSUE-Placenta;
A Satto K., Yamamoto J., Wakamateu A., Nagai T., Nakamura Y.,
A Satto K., Yamamoto J., Wakamateu A., Nagai T., Nakamura Y.,
A Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
E EMBL; AKO75445; BAC11626.1;
R InterPro; IPR000884; TSP1.
R Pfam; PF007081; AKO7845; AMOP.
R Pfam; PF007081; AKO7845; AMOP.
R Pfam; PF007081; AKO791:
R SMART; SM00729; ANOP.
R SMART; SM00729; TSP1:
R SMART; SM00209; TSP1:
R PROSITE; PS50092; TSP1: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 LPVKKPRLKGPRPGSLTRLAEVSASPDPRPLKEEBEAPLLPRTHLQAEPHQHGCWTVTEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 995; DB 2; Length 571; Best Local Similarity 100.0%; Pred. No. 1.5e-58; Matches 187; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63919 MW; 06079153C433D28C CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
11-0CT-2002 (TrEMBLrel. 26, Last annotation update)
Hypotherical protein PSEC0137.
Homo sapiens (Human)
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YD53
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Q95LR6
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                                                                                                                                                                                                                                              1 LPVKKPRLRGPRPGSLTRLA......PELVHATLSTPNPDNQVTIK 187
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               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length DB
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120

9 86

Gaps

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Best Local Similarity 98.9
Matches 185; Conservative
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
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Pfam; PF00090; TSP 1; 1.
SMART; SM00723; AMOP; 1.
SMART; SM00209; TSP1; 1.
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571 AA;
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Best Local Similarity
Matches 185; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
Full-length cDNA 5-PRIME end of clone CS0DI033XJ09 of Placenta of Homo sapiens (human) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 AAMTPGNITPPRIPEVTPENTELQKLPGLANITISTPNPDIQASASPDPRPLREEEEARL
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                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens (human) (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                          Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Pobo G., Han M., Wiemann S.; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR749863; CAH18707.1; -.
InterPro; IPR005533; AMOP.
InterPro; IPR00884; TSP1.
Pfam; PF00309; TSP 1.
Smarr; SM00723; AMOP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.7%; Score 992; DB 2; Length 57 Best Local Similarity 99.5%; Pred. No. 2.3e-58; Matches 186; Conservative 1; Mismatches 0; Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248770; CAD66577.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jessee J., Polayes D.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                       578 AA; 64611 MW; 4BA9FA46801BD68B CRC64;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein DKFZp686E0215 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 AA.
                                                                                                                                                                             The German cDNA Consortium;
                                                                                                                                                                                                                                                                                                                                          PS50092; TSP1; 1
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                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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Li W.B., Gruber C., J
Submitted (FEB-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 DNOVTIK 220
                                                             Name=DKFZp686E0215;
                                                                                                                                                  SEQUENCE FROM N.A.
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TISSUE=Placenta;
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                                                                                                                                                                   rissum=Cervix
                                                                                                                                                                                                                                                                                                                                                                       NON TER
SEQUENCE
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150
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                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LPRTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 180
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                                                                                                                                                                                                                                                   1 IPVKKRIRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEP
                                                                                                                                                                                                                                                                                                                                                            91 AAMTPGNATPPRTPEVTPLKLELQKLPGLANTTLSTPNPDTQASASPDPRPLREEEEARL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Heart;
Rossi V., Beffagna G., Rampazzo A., Bauce B., Danieli G.A.;
Rossi V., Beffagna G., Rampazzo A., Bauce B., Danieli G.A.;
Rossi V., Beffagna G., Rampazzo A., Bauce B., Danieli G.A.;
Rossi V., Beffagna G., Rampazzo A., Bauce B., Danieli G.A.;
and AMOP domain, mapped to ARVD1 critical region.";
Gene 335:101-108(2004).
EMBL; AJ583024; CAE47313.1;
InterPro; IPR005533; AMOP.
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5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
65-JUL-2004 (TrEMBLrel. 27, Last sequence update)
77, Last sequence and action update)
Thrombospondin and AMOP containing isthmin-like 1 protein, (Taill)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                        Length 328;
                                                                            99.2%; Score 987; DB 2; Length 32/
98.9%; Pred. No. 2.8e-58;
... wiematches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
1 1
328 328
328 AA; 36307 MW; 56C700854F62E89B CRC64;
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571 Taill protein.
63906 MW; D83329D10F300C7C CRC64;
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Hypothetical
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147 LPRTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP 206
                                                                                                                                                                                                                                                                                                                                                                                                                          88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 LPRTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNP
                                                                                                                                                                                                                                                                                                                                                                                                    1 LPVKKPRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEP
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-GT-2003 (TrEMBLrel. 25, Last annotation update)
Full-length cDNA clone CSODI014TN05 of Placenta of Homo sapiens (human) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                           Length 294;
                                                                                                                                                                                                                                                                                                                                                           97.4%; Score 969; DB 2; Length 29
98.9%; Pred. No. 3.9e-57;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                             Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX248277; CAD62605.1; -...
NON_TER 1
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                       SEQUENCE 294 AA; 31563 MW; 5127610A07112FC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         658 AA
                                                                                          294 AA
                                                                                          PRT;
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Best Local Similarity 98.9
Matches 181; Conservative
                                                                                          PRELIMINARY;
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                   DNOVTIK 187
                                      207 DNÓVTIK 213
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Li W.B., Gruber (
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Stardchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villadon D.K., Muzny D.M., Sodergren B.J., Lu X., Glibs R.A.,
A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 EEEAPLLPRTHLOAEPHOHGCWTVTEPAAMTPGNATPPRTPEVTPLRLELOKLPGLANTT
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 93.8%; Score 933.5; DB 2; Length 658; Best Local Similarity 67.5%; Pred. No. 2.1e-54; Matches 185; Conservative 1; Mismatches 1; Indels 87;
           Group;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ll protein.
658 AA; 72519 MW; 7EIDF224645B300F CRC64;
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Last annotation update)
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UW Multimegabase Sequencing Gr
Submitted (DRC-1998) to the EM
EMBL; AF111168; AAD09622.1; -
Genew; HGNC:23176; THSD3.
InterPro; IPR005533; AMOP.
InterPro; IPR00884; TSP1.
Pfam; PF003782; AMOP; 1.
SMART; SM00723; AMOP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THSD3 protein (Fragment).
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 PRPIKEEEEAPILPRIHILOAEPHOHGCWIVIEPAAMITPGNATPPRIPEVIPIRIELOKLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRLELQKLP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODI024YA19 of Placenta of Homo sapiens (human) (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.6%; Score 842; DB 2; Length 51 98.1%; Pred. No. 2.18-48; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Placenta;
Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases
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308 AA; 34735 MW; 38F47CC67F7D44E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 AA; 58281 MW; EB6BB57C4D44E928 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 NATPPRIQEVIPLILELOKIPELVHATLSTPNPDNOVTIK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NATPPRIQEVIPLALELQKLPELVHATLSTPNPDNQVTIK 160
                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      308 AA.
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                                                                                                                                                                                     Strausberg R.;
Submitted (JUN-2002) to the EM EMBL. BC03140, AAH33140.1;
Interpro; IRR005633; AWOP.
Interpro; IRR006884; TSP1.
Ffam; PP007887; AWOP; 1.
SFAMT; SM00703; AWOP; 1.
SWART; SM00703; AWOP; 1.
SWART; SM00709; TSP1; 1.
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InterPro; IPR005533; AMOP.
InterPro; IPR000884; TSP1.
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Pfam; PF00090; TSP 1; 1.
SMART; SM00209; TSP1; 1.
PROSITE; PS50092; TSP1; 1.
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                                    sednences
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Best Local Similarity
Matches 60; Conserv
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                                                                                                                               SECUENCE FROM N.A.
                                                                                                                                                                 TISSUE=Placenta;
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                              mouse cDNA
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0.0867W4
1.D 0.0867T
1.D 0.067T
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1.D 0.067T
1.D 0.067T
1.D 0.067T
1.D 0.01-M
1.D 0.1-M

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72 RIPEVIPLRIELOKIPGIASTILSTPNPDIQASASP----DPRPLREEEEARLLPRIHLQ 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         555 ТТТКЕРАРТТРКЕРАРТТРККРАРТТРКЕРАРТТРКЕРАРТТТККРАРТАРКЕРАРТТРК 614
128 AELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNPDNQVTIK 187
                                   1 AELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNPDNQVTIK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Turner K.J., Fitz L.J., Temple P., Jacobs K., Larson D., Leary A.C.,
Kelleher K.J., Giannotti J., Calvetti J., Fitzgerald M., Kriz M.J.,
Ferenz C., Grobholz J., Fraser H., Bean K., Norton C.R., Gesner T.,
Bhatia S., Kriz R., Hewick R., Clark S.C.;
"Purification, Biochemical Characterization, and Cloning of a Novel
Megakaryocyte Stimulating Factor that has Megakaryocyte Colony
Stimulating Activity.";
Blood 78:279-279(1991).
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Genew, HGNC:9364; PRG4.
GO; GO:000283; Prc-11 proliferation; TAS.
InterPro; IPR001212; Somatomedin_B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mosher D.F. (eds.);
BIOLOGY OF VITRONECTINS AND THEIR RECEPTORS., pp.45-52, Elsevier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP00045; Hemopexin; 2. Pfam; PP00045; Hemopexin; 2. Pfam; PP01033; Somatcomedin B; 2. PR1NTS; PR00022; SOMATOMEDINB. SMART; SM00120; SO; 2. SMART; SM00201; SO; 2. PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1. PROSITE; PS00024; SMB 1; 2. SEQUENCE 1404 AA; 151090 MW; AABD7AD19B35F4F6 CRC64;
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                                                                                                                                                                                                                                                                                                        01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                           PRT; 1404 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               Megakaryocyte stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science Publishers B.V. (1993).
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                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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675 NTPKEPAPTTPKEPAPTTPKETAPTTPKGTAPTTLKEPAPTTPKRAPAP 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---- PGNTTPP
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Eukaryota; Metazoa; Atth. PEST.
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 SASPDPRPLKEEERAPLLPRTHLQAEPHQHGCWTVTEPAAMT-----
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PROSITE; PS00524; SMB 1; 2.
SEQUENCE 1404 AA; I51076 MW; 782A11746B3FDEE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wray P.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL133553; CAC36090.1; -.
HSSP; P04004; 10C0.
                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
BG174L6.2 (MSF: megakaryocyte stimulating factor).
Name=bG174L6.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 26, Created)
(TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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Name=agCG56847; ORFNames=ENSANGG0000018269;
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                                                                                                                                                                                                                                                              Created)
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InterPro; IPR001212; Somatomedin_B.
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Pfam; PF01013; Somatomedin B; 2.
PRINTS; PR000022; SOWATOMEDĪNB.
SWART; SM00120; HX; 2.
SWART; SM00201; SO; 2.
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                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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01-MAR-2004
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Matches
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Q7QFG1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 PSTNIPLT--------TPGSTTPKPTPEPSTIIPLTTPGSATSEVTPE 460
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-!- SUBCELLULAR LOCATION: Concentrated at presynaptic side of synaptic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 PRPGSLTRLAEV-SASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAM----TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH RABACI.
MEDLINE-20170257; PubMed=10707984; DOI=10.16/S0896-6273(00)80883-1;
Fenster S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B.,
Garner A.M., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.;
"Piccolo, a presynaptic zinc finger protein structurally related to bassoon.",
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALICUM-BINDING ACTIVITY, AND MUTAGENESIS OF ASP-4668; ASP-4674; 468-4689; 4689-WAL-4689; 4689-WAL-MET-4669; MET-4689; 4690-VAL-4691; 462-GLN-ASN-4693 AND ALA-4694.

MEDLINE=21181819; Pubmed=11285225; DOI=10.1093/emboj/20.7.1605; Gerber S.H., Garcia J., Rizo J., Suedhof T.C.; An unusual C(2)-domain in the active-zone protein piccolo: implications for Ca(2+) regulation of neurotransmitter release."; EMBO J. 20:1605-1619(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
Fenster S.D., Cases-Langhoff C., Gundelfinger B.D., Garner C.C.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9JKSG, Q9JLT1;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Piccolo protein (Multidomain presynaptic cytomatrix protein).
                                                                                                                                                                                                                                                                                                                              13.3%; Score 132; DB 2; Length 837; 27.6%; Pred. No. 0.71; ative 24; Mismatches 60; Indels
                                                                                                                                                                                                                                                                837 AA; 85371 MW; C506EF34EF2A726B CRC64;
GO, GO:0005576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:0006030; P:chitin metabolism; IEA.
InterPro: IPR002557; Chitin bind PerA.
Pfam; PF01607; CBM 14; S.
PROSITE; PS50940; CHIT_BIND_II; S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-VHATLSTPNPDNQVTIK 187
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                                                                                                                                                                                                                                                                                                                                                                Local Similarity 27.69
ses 55; Conservative
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                                                                                                                                                                                                                                 837
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@18b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ON->AA: Moderate increase in affinity for calcium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure; Alternative splicing; Calcium/phospholipid-binding;
Metal-binding; Repeat; Zinc; Zinc-finger.

DOMAIN 372 491 12 X 10 AA tandem approximate repeats of P-A-K-P-Q-P-C-Q-P-X.

ZN FING 523 547 C4-type (Potential).

ZN FING 1010 1033 C4-type (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M->S: Increased affinity for calcium. VV->SS: 10-fold increase in affinity for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VM->SS: 10-fold increase in affinity for
                                                                                                                                                                                                                                                                                                                                           R GO; GO:0005502; C:synapse; IDA.

R GO; GO:0005524; F:calcium ion binding; IDA.

R GO; GO:0005544; F:calcium dependent phospholipid binding; IDA.

GO; GO:0005524; F:profilum binding; ISS.

R GO; GO:0005525; F:profilum binding; ISS.

R GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.

R GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.

R O; GO:000008; CS:

R InterPro; IPR0001478; PDZ.

R InterPro; IPR0001499; ZI.

R Pfam; PF00169; PDZ; 1.

R Pfam; PF00169; C2; 2.

R Pfam; PF00159; C2; 2.

R RMART; SM00239; CZ: 2.

R RMART; SM00218; CZ: DOMAIN 1; 1.

R PROSITE; PS50016; PDZ; 1.

R PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D-5A: Complete loss of calcium-binding and calcium-dependent phospholipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Complete loss of calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and calcium-dependent phospholipid binding activity. V->S: Small increase in affinity for
                                                       Isole-09JK86-2; Sequence-VSP 003930, VSP 003931;
DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change. SIMILARITY: Contains 2 C2 domains. SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A->S: No effect on calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKPTN -> SKRRK (in isoform 2)
/FTIGa-VSP 003930.
Missing (In isoform 2).
/FTIGa-VSP_003931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity.
5085 AA; 552702 MW; SAIBB543201A7450 CRC64;
Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain 1.
domain 2.
                  Name=1;
IsoId=Q9JKS6-1; Sequence=Displayed;
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                                                                                                                                                                                                                                                                                   EMBL; AF138789; AAF07822.2; -.
EMBL; AF227534; AAF63196.1; -.
PDB; 1RH8; NMR; A=4635-4776.
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                                                                       63 MIPGNITPPRIPEVIPLRLELQKLPGLASTILSTPNPDIQASASPDPRPLREEEEARLLP 122
                                                                                                                            123 RTHLQAELHQHGCWTVTEPAALTPGNATPPRTQEVTPLLLELQKLPELVHATLSTPNPDN 182
                                                                                                                                                                                     : |: : : : | | | | : | | 3.8PIKTD-----SAKPSQSFPPTGEKTTPLDSKAMPRPASDSKIISQPGPGS 789
                                                    3 VKKPRLRGPRPGSLTRLAEVSASPDPRPLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAA
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Rhabditidae; Peloderinae; Caenorhabditis.
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                          49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
Length 5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.4%; Score 123; DB 2; Length 880; 26.9%; Pred. No. 3; tive 14; Mismatches 62; Indels
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AR026205, ABR71258.1; -.
ENRL, D89756, D89756.
Wormbase; WBGene00020732; T23E7.2.
Wormbep; T23E7.2b; CE14066.
Hypothetical protein.
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Latreil P., Stellyes L., Elliot G., Wilson R., "The sequence of C. elegans cosmid T23E7."; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein T23B7.2.
ORFNames=T23B7.2, T23B7.2,
Caenorhabditis elegans.
 DB 1;
                            63;
                                                                                                                                                                                                                                                                                                                              880 AA.
Query Match 12.5%; Score 124.5; Best Local Similarity 23.2%; Pred. No. 15; Matches 42; Conservative 27; Mismatches
                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 26.9%
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.;
Submitted (NOV-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WormBase Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Bristol N2;
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                                                                                                 -----TILSTPNPDIQASASPDPRPLREEEBARLLPRIHLQAELHQHGCWTVTEPA 142
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                                             392 EETPATPRSSVPATPTES---NLTTPAPKTPKTPKTPRTPR-TPKTPKTPKTPAVVEPEP 447
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EEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNTTPPRTPEVTPLRLELQKLPGLAS---
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01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
01-NXY-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
0RFNames=723E7.2, T23E7.2, Caenorhabditis elegans.
Caenorhabditis elegans.
Bluarycla: Metazoa; Nematoda: Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                        143 ALTPGNATPPRTQEVTPLLLE--LQKLPELVH-----ATLSTPNP 180
                                                                                                                                                                                                                                     PAADETATEPTAEEAEPEAVEESIEK-TEVVEEESAPPAARQSSPSP 533
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26.9%; Pred. No. 3;
tive 14; Mismatches 62; Indels
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Latrell P., Stellyes L., Elliot G., Wilson R.;
"The sequence of C. elegans cosmid T23E7.";
Submitted. (OCT.-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    448 EPVAEEPEPVAEPEPEPEPVAEAEPEAEPAVEEPAE------
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EMBL, AF026205, AAD47129.1; -.
WormBase, WBGene00020732; T23E7.2.
WormPep; T23E7.2c; CE24007.
Hypothetical protein.
SEQUENCE 885 AA; 96409 MW; 0AB.
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MEDLINE=99069613; PubMed=9851916;
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Best Local Similarity 26.9
Matches 45; Conservative
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STRAIN=Bristol N2;
Wilson R.;
Submitted (DEC-2003) t
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Submitted (NOV-2002)
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                 538 PAADETATEPTAEEAEPEAVEESIEK-TEVVEESAAPPAARQSSPSP 583
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143 ALTPGNATPPRIQEVTPLLLE--LOKLPELVH-----ATLSTPNP
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STRAIN=Bristol N2;
Latrail P., Stellyes L., Elliot G., Wilson R.;
"The sequence of C. elegans cosmid T23E7 ";
Submitted (CCT-1997) to the EMBL/GenBank/DDBJ databases.
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Wormbase; WBGene00020732; T23B7.2.
Wormbcp; T23E7.2e; CE31244.
Hypothetical protein: SEQUENCE 908 AA; 98283 MW; 11C0CD0C7EA6F0E4 CRC64;
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Hypothetical protein T23E7.2.
ORFNames=T23E7.2, T23E7.2;
Caenorhabditis elegans.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Hayashi,K.
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Patent: EP 1067182-A 153 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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Seguence 153 from Patent BP1067182.
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/mol type="unassigned DNA"
/db xref="taxon:9606"
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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BD093285 Different
BD123568 Secretory
AK075445 Homo sapi
                                                                                     February 22, 2005, 00:06:56 ; Search time 2780 Seconds (without alignments) 3259.398 Million cell updates/sec
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                             nucleic search, using frame_plus_p2n model
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       Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Yoshida,K. and Masuho,Y Differentiation growth factor Patent: WO 0104312-A 1 18-JAN-2001; HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI,KENIY YOSHIDA,YASUHIKO MASUHO OS HOMO Bapiens (human)
                                                                                                                                                                              TASUHIKO MASUHO
C12N15/16,C12N15/12,C12N15/85,C12N5/10,C12P21/02,C07K14/575,
C07K14/72,
C12Q1/68,C12Q1/02,A61K67/027//(C12P21/02,C12R1:91) CC

Key
(58) . (1770) .
Location/Qualifiers
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//mol_type="genomic DNA"
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WSPCSGNCSTGKQQRTRPCGYGCTATETRTCDLPSCPGTEDKDTLGLPSEFWKLLARN
ATDMHDQDVDSCEKWLWCKSDFLIKYLSQMLRDLPSCPGTEDKDTLGLPSEFWKLLARN
RSFRWRDASGPRERLDIYQPTARFCLRSWLSGESSTLAAQHCCYDEDSRLITRGKGA
MPNLISTDFSPKLHFKFDTTPWILCKGDWSRLHAVLPPNNGRACTDNPLEEEVLAGLG
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Differentiation growth factor.

Differentiation growth factor.

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GI:22638873

WO 0104312-A/1.

Homo sapiens (human)

Homo sapiens (human)

Homo sapiens (bumato)

Homo sapiens (human)

Mono sapiens (human)

Homo sapiens (human)

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Ota,T., Nishikawa,T., Suzuki,Y., Kawai-Hio,Y., Hayashi,K.,
Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.,
HI human cDNA sequencing project

L Unpublished

S Isogai,T. and Yamamoto,J.

S Isogai,T. and Yamamoto,J.

Direct Submission

Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Direct Submission

Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3965)

HRI human cDNA sequencing project; cDNA 5- & 3' end one pass
Sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.);
CDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center.
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SEDI BGEDQEDKEEDEEEQALWFNGTTDNWDQGWLAPGWYFKDSVSYDYEPQKEWSP
WSPCSGNCSYGKQQRTRPCGYGCTATTDNWDQGWLAPGWYFKDSVSYDYEPGKEWSP
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/tissue type="placenta"
/tissue Tib="PLACE1"
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/note="unnamed protein product"
/codon start=1
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                          964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2981)
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07-JUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
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Hayashi,K.
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Secretory protein or membrane protein
FH Key Location/Qualifiers
FT CDS (58). (1770)
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Conservative:
Mismatches:
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Patent: JP 2002017376-A 77 22-JAN-2002;
HELIX RESBARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017376-A/77
                                                                                                                                                                                      Secretory protein or membrane protein. BD123568
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                             BD123568.1 GI:23218513
JP 2002017376-A/77.
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Homo sapiens
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Best Local Similarity:
Query Match:
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1 protein, (Taill)"
/protein id="CAE47313.1"
/bc.xref="CI:48958175"
/translation="WRALRIPS"
LABVSASPDERPLKYEEERAPLLERTHLQAEPHQHGCWTVTEPAAMTPGNATPPRTPEV
TPLRLELQKLPGLANTTLSTPNPDTQASASPDPRPLEEEERRLLPRTHLQAELHQHG
                                                                                                                                                                                                                                                                                                                                                                                                                CWTUTEPALTPGNATPPRTOEUTPILLELOKLPELVHATLSTPNPDNQVTIKVVEDP
OSAVSTOLLARENNPPROTOTISMLPAMSFLWGODYKGERKDDEDDY
SEDTSEEDOEDKEBERDALWFOTTNUMDGWLAFGDWVFKDSVSYDYEPQKEWSP
WSPCSGNCSTGKQORTRPCGYGCTATETRTCDLPSCPGTEDKDTLGLPSEBKILLARN
ATDMINODNOSCEKWINKSPPLIKYLSQWLWPLSSCPGTEDKDTLGLPSEBKILLARN
RSFWRDASOPRELLDIYQPTARFCLRSMLSGSESSTLAAQHCCYDBDSRLLTRGKGAR
MPNLISTDFSPKLLTPRTOTPWILCKGDWSRLHAVLPPNNGRACTDNPLEEEYLAQUO
                                                                                                                                                                                                                                                                       /codon_start=1/product="thrombospondin and AMOP containing isthmin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 GAGGTCTCAGCCTCCCCAGATCCTAGAGCTCTCTGAAGAAGAAGAGGAGGAGGAGCACCACTGCTC
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Location/Qualifiers
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/organism="Homo sapiens"
                                                                                                                      /man="14624.3"
/tissue_type="heart"
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1. .2883
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                                                                     /mol_type="mRNA"
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gene="TAIL1"

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/gene="TAIL1"

/product="TAIL1"

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/gene="TAIL1"
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Direct Submission
Submitted (16-SEP-2003) Rossi V., Department of Biology, University
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                              LeuProValLysLysProArgLeuArgGlyProArgProGlySerLeuThrArgLeuAla
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REFERENCE AUTHORS ISOGAI,T., Octsuki,T. and Sugiyama,T. TITLE Direct Submission JOURNAL Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hiri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, CDNA full insert sequencing: Research Association for Blotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5 £ 3end one pass sequencing: RAB, HRI, and Biotechnology Center tc.); 7 £ 3end one pass sequencing: RAB, HRI, and Biotechnology Center of tull insert sequencing: RAB and HRI. Location/Qualifiers BOUNCE 1. 3052	/ Ordanism="Homo sapiens" / (a)	00 00 00 00 00 00 00 0
Qy 121 LeubroArgThrHisLeuGlnAlaGluLeuHisGlnHisGlyCysTrpThrValThrGlu 140 Db 474 CTCCCCAGAACCCACCTGCAGGCAGGCTACACCAACATGGATGTTGGACTGTCACTGAG 533 Qy 141 ProAlaAlaLeuThrProGlyAsnAlaThrProProArgThrGlnGluValThrProLeu 160 Db 534 CAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCAGGACCTACTCCCTTG 593 Qy 161 LeuLeuGluLeuGlnLysLeuProGluLeuValHisAlaThrLeuSerThrProAsnPro 180 Db 594 CTGCTGGAGCCCAGAGCTGCCAGAATTGGTCCACGCACCTTGAGTACTCCCTTG 593 Qy 161 LeuLeuGluLeuGlnLysLeuProGluLeuValHisAlaThrLeuSerThrProAsnPro 180 Db 594 CTGCTGGAGCTGCAGAATTGGTCCACGCAACCTTGAGTACCCTAACCCT 653 Qy 181 AspAsnGlnValThrIleLys 187 Db 654 GATAACCAGGTGACCATCAAG 674	RESULT 6 AKO56709 AKO567	Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komateu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nakai, K., Nakahashi, Y., Nakagawa, K., Okumura, R., Nakai, K., Yamashita, R., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S. Complete sequencing and characterization of 21,243 full-length human cDNAs JOURNAL Nat. Genet. 36 (1), 40-45 (2004) NAT. Genet. 36 (1), 40-45 (2004) REFERRNCE Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Authors, A. Takahashi-Fujii, A., Tanase, T., Irie, R., Otsuti, T., Sato, H., Wakamateu, A., Ishii, S., Yamashita, H., Natamata, T., Irie, R., Otsuti, T., Sato, H., Wakamateu, A., Ishii, S., Yamashita, H., Watana, H., Sugiyama, T., Ishii, K., Mata, H., Sugiyama, M., Makamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Mata, H., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. TITLE NEDO human cDNA sequencing project Unpublished

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Homo sapiens (Lichard) Fordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E. 1 (Dases 1 to 2783)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., RAusmer, C.M., Schmer, C.M., Schmer, C.D., Altschul, S.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstain, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bossak, S.A., McEwan, P.J., McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, J., Helton, B., Sedergren, B.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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                                                                                                                                                                              GluvalSerAlaSerProAspProArgProLeuLysGluGluGluGluAlaProLeuLeu
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                                                                                          LeuGluLeuGlnLysLeuProGlyLeuAla-SerThrThrLeuSerThrProAsnProAs 100
                                                                                                                   CTGGAGCTGCAGAAGCTGCCGGGATTGGCCAAACAACCTTGAGTACCCCTAACCCTGA 435
                                                                                                                                                                                                   TACCCAGGCTTCAGCCTCCCCAGATCCTANGCCTCTGAGGGAAGAGAGGAGGAGGACGACT 495
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Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
                  aAlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArg
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/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
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61 GAGCCACACCAAACATGGATGCTGGACTGTCACTGAGCCAGCAGCATGACCCCAGGCAAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 AATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGGAGCTGCAGAAGCTG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GATCCTAGGCCTCTGAGGGAAGAGGAGGAGCACGACTGCTCCCCAGAACCCACCTGCAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 ProGluLeuValHisAlaThrLeuSerThrProAsnProAspAsnGlnValThrIleLys 187
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1 (bases 1 to 231464)

Multimegabase Sequencing Group.

Complete sequence of the gene for serine palmitoyltransferase, subunit II found on human chromosome 14
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                                                                                                                                                                                                                                                                                                                        48 GluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThrProGlyAsn
                                                                                                                                                                                                                                 1 CCTAGGCCTCTGAAGGAAGAAGAGGAGGAGGCACCACTGCTCCCCCAGAACCCACCTGCAGGCA
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                                                                                                                                                                                     ProArgProLeuLysGluGluGluGluAlaProLeuLeuProArgThrHisLeuGlnAla
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Direct Submission
Submitted (27-DEC-1998) Department of Molecular Biotechnology,
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                                                                                                                    (1-2783)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obl Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Parvanch Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Bubane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LiNL at: http://image.llnl.gov Series: IRAL Plate: 43 Rows: c Column: 10.
Location/Qualifiers
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, J., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length minan and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (125-UN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       choriocarcinoma"
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157
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Matches:
Conservative:
Mismatches:
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nol_type="mkN"
db_xref="taxon:966"
/clone="IMAGE:3844836"
fissue type="Placenta, ch
/clone_lib="NIH MGC_21"
/lab_host="blub"=R"
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db xref="LocusID:145501"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene="THSD3"
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98.12%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                       Strausberg, R.
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Best Local Similarity:
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FEATURES

CDS

ORIGIN

Score:

PRI 14-JUL-1999

Box

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/ In the complement (1824. 18306) / rpt family="LiMB1" complement (18310. 18609) / rpt family="AllaSx" complement (18624. 18771) / rpt family="LiMB3" complement (18765. 18847) / rpt family="LiMB3"
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/rpt family="Alusq"
complement (22042...2342)
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complement (22350...22937)
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complement (2350...23090)
/rpt family="FLAM_C"
complement (23164...23287)
/rpt family="Lalus"
/rpt family="Lalus"
/rpt family="Lalus"
/rpt family="Lalus"
/rpt family="Lalus"
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complement(14884. .14905)
'rpt_family="AT_rich"
complement(15106. .15393)
/rpt_family="AluSx"
complement(15606. .15818)
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/rpt family="AluJb"
complement (21030. 21122)
/rpt family="(TAAA)n"
complement (21125. 21423)
/rpt family="AluJo"
/rpt family="AluJo"
/rpt family="(11491) family="(11491)
/rpt family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) family="(11491) fami
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/rpt family="LIMB2"
/rpt family="AluSx"
/rpt family="AluSx"
/rpt family="(TAGA)n"
                                                        family="LIME2"
ement(1=0.000)
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rpt family="Alusc"

omplement (16775. 17073)

rpt_family="Alux"
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complement(19503..20417)
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complement (20104. .20625)
/rpt_family="L143_5end"
complement (20724. .21029)
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14795. .14857
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--/14884. .1
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12746. 12920
/rpt_family="BC200"
13931. 13217
/rpt_family="AluSx"
13236. 13751
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14405. .14717
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rpt_family="FLAM_C"
              1800. .12161
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3783. .14084
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                                            /rpt_family="Theic
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omplement(17815.
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7708. 8007

8233. 8305

/rpt_family="AluSx"

8233. 8305

/rpt_family="(TA)n"

9186. 9230

/rpt_family="(CA)n"

complement(join(9248. 9470,10060. .10240,16529. .16722,

25330. .25484))

/note="Intron-exon boundaries defined in relation to an

EST contigs that includes A4397580, A1138314, A4399545,

AA868184, all from testis. The closest match in BLASTX is

to E. coli pyrroline-5-carboxylate reductase."
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/rpt family="AluJb"
complement (11156. 11306)
/rpt family="MRR"
complement (11493. 11615)
                                                                                                                                                                                                                        2059. .2834
/rpt_family="L191_Send"
complement(2937. .3255)
/rpt_family="MER4A"
3323. .3687
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ement(1)000
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/note="low quality data"
complement(6914. .7458)
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/rpt_family="LiMC1"

5350 . 5650

/rpt_family="AluSq"

5868 . 5924

/rpt_family="(TAAAA)n"

5869 . 5940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omplement (6500. .6588)
rpt family="58"
omplement (6715. .6815)
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.086. .6271
                                                                             /rpt_family="AluSg"
1284. .1581
/rpt_family="AluSg"
1582. .1774
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/rpt_family="AluJb"
2059, .2914
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/rpt_family="AluSp"
5238, .5349
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/ kpc. family="Alusg"

4009 ... 4314

/ kpc. family="AluJo"

4321... 4934

/ kpc. family="L1"

4940... 5536
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complement(10461...1
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family="AluJb"
                                     rpt_family="AluSx"
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523. .7707
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rpt_family="L1MB6"
rpt_family="L1MD1"
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PAT 19-JAN-2004
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                                                                                                                                                                                      Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
Patent: WO 0157270-A 161 09-AUG-2001;
Aeomica, Inc. (US)
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/rpt family="MER20"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived slingle exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157272-A 166 09-AUG-2001;
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Sequence 166 from Patent WO0157272.
CQ091307
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Location/Qualifiers
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                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                      for
                                                                                                                                                                                            Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelialcells
Patent: WO 0157278-A 165 09-AUG-2001;
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                                               DNA
                                        Sequence 165 from Patent W00157278.
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Location/Qualifiers
                                                                                           CQ064365.1 GI:41034232
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658.50
76.97%
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             RESULT 13
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Job time : 2828 secs

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/organism="Homo sapiens"
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= 0.92"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                           Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
Patent: WO 015/276-A 163 09-AUG-2001;
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            linear
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     Sequence 163 from Patent W00157276.
CQ130141
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Location/Qualifiers
                                                CQ130141.1 GI:41087497
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Adk67917 Human ext.
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Ad113810 Osteoarth
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Aca64826 Human meg
Add12655 Human cDN
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Adi31655 Human cDN
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Aai31480 1
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ABS38283
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AAK38709
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P-PSDB; AAB49765.
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18-OCT-1999;
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Aaf93820 Human cDN
Aaf94019 Primer sp
Aai10232 Probe #16
Aba51868 Human foe
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Listing first 45 summaries
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                                                                                                                                  drugs
                                                                               This invention relates to polynucleotide sequence PSEC137, which encodes a human proliferation differentiation factor protein. Included in the invention is a vector containing the cDNA sequence, a transformant containing the vector, and a process for producing the protein. The protein together with its encoded DNA and antisense DNA are used in drugs to maintain the haematopoietic function. The present sequence represents cDNA encoding the proliferation differentiation factor protein
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     Proliferation-differentiation factor protein encoded by PSEC137 cloned from human cDNA library, being hematopoietic factor for inducing differentiation of blood cells, used to maintain hematopoietic function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AlaAlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArg
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unds invention relates to indicate acts bequeices and single and which encode human secretory or membrane proteins represented by AAB88317

AAR88419. Included in the invention are primers AAF93317 - AAF94295 and AAF884212 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF623 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF62213 - AAF623 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - AAF62313 - 
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                                  Human cDNA encoding a membrane or secretory protein clone PSEC0137.
                                                                         Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention relates to nucleic acid sequences AAF93744
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00183766.
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                                                  LeuleuGluleuGlnLysLeuProGluleuValHisAlaThrLeuSerThrProAsnPro
                                                                                                                                                                                            316 GCAGCCATGACCCCAGGCAACACCACCCTCCCAGGACCCCAGAGGTTACTCCGTTGCGG
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61 AlaAlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                  496 ICTCCCCAGAACCCACCTGCAGGCAGAGCTACACCCAACATGGATGTTGGACTGTCACTGAG
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11-JAN-2000; 2000JP-00118775.
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AAF62232 - AAF62235 which are used to isolate the CDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polymucleotide sequences can be used in gene therapy. The polymucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of disagnses associated with inappropriate secretory protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR) to detect and quantitate the presence of similar nucleic acid sequences in samples. They may also be used as antigens in the production of antibodies polypeptides may be used as antigens in the production of antibodies adainst them and in assays to identify modulators (agonists and antagonists) of expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also be used as therapeutic agents to down regulate expression and activity. Examples (e.g. by enzyme treated include rheumatoid arthritis and diabetes
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                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgThrProGluValThrProLeuArgLeuGluLeuGlnLysLeuProGlyLeuAlaSer 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 HisGlyCysTrpThrValThrGluProAlaAlaMetThrProGlyAsnThrThrProPro
                                                                                       expression analysis in human cervical cell sample.
                                                                                                         human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
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126
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                Claim 25; SEQ ID NO 165; 487pp; English
                                                                                                                                                                                                                                                                                                                            Chen W, Rank DR
                                                                                                                                                                                                                                                                                                        (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                   26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
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27-SEP-2000; 2000US-0236359P.
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658.50
76.97%
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                              AAI10232 standard; DNA; 497
                                                                      (first entry)
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                                                                                          #165 for gene
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                                                                                                                        cervical cancer; ss
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Best Local Similarity:
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                   196 TCACCTTCCCTCTCTCTCAGCTTCAGCCTCCCCAGAICCTAGGCCTCTGAGGGAA
                                                                                                                                                                                                                                                                                                                                                       CysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArgThr
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ThrThrLeuSerThrProAsnProAspThr
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26-MX-2000; 2000US-0207456P.
30-UJN-2000; 2000US-00608408
03-AUG-2000; 2000US-0053366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
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ABA21690 standard; DNA; 497
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27-SEP-2000;
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              U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis;
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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                                                                                 The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71
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                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 166; 654pp; English.
                                                                                                                                           Chen W, Rank DR
                                                                                                                                                                                                                                            gene expression in human placenta.
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                                                                                                   (MOLE-) MOLECULAR DYNAMICS INC.
2000US-00632366.
2000US-0234687P.
2000US-0236359P.
                                                          04-OCT-2000; 2000GB-00024263
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single exon nucleic acid probes for analyzing gene expression in human
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                                                                             expression analysis in human heart cell sample
                                                                                                           Human, gene expression; heart, microarray, vascular system; probe, cardiovascular disease, hypertension; cardiac arrhythmia; congenital heart disease; ss.
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2000US-00608408.
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03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
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                                                                                                                                    196 TCACCTTCCCTCTCTCTCAGGCTTCAGGCTCCAGAICTAGGCCTCTGAGGGAA 137
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                                                                                       CCTGGCTCTGCCTGGCCTTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCACC 197
                                                                                                                                                                                                             77
                                                                                                                                                                                                                                                           -----GlnAlaSerAlaSerProAspProArgProLeuArgGlu
                                                                                                                                                                                GluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHisGly
                         <u> ACAACCTTGAGTACCCTAAACCCTGATACCCAGGTGAGAGGTTACAGAAGGGCCCAGCAGCT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bone marrow expressed single exon probe SEQ ID NO: 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
 ThrThrLeuSerThrProAsnProAspThr
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2000US-0207456P.
2000US-00608408.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
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English

+ Sequence Listing;

R Rank

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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the invention
                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                 Sequence 497 BP; 81 A; 128 C; 177
                                                                                                                                         Example 4; SEQ ID NO 158; 650pp
                                                               Chen W,
                                          (MOLE-) MOLECULAR DYNAMICS INC
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                   WPI; 2001-483446/52
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Best Local Similarity:
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Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
ss.
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                                                                                                                 LysGluGluGluGluAlaProLeuLeuProArgThrHisLeuGlnAlaGluProHisGln
                                                                                                                                                            HisGlyCysTrpThrValThrGluProAlaAlaMetThrProGlyAsnThrThrProPro
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                    497
126
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                                                                                             x AAK25606 (1-497)
                  Length:
Matches:
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|ThrThrLeuSerThrProAsnProAspThr
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                    4.11e-31
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          Scores:
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G; 111 T; 0 U; 0 Other;
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                                                          Length:
Matches:
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                                                          4.11e-31
658.50
76.97%
76.36%
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316 ACAACCTTGAGTACCCCTAACCCTGATACCCAGGTGAGAGCTACAGAAGGGCCAGCAGCT

92 ThrThrLeuSerThrProAsnProAspThr -----

5

72 ArgThrProGluValThrProLeuArgLeuGluLeuGlnLysLeuProGlyLeuAlaSer

256 CCTGGCTCTGCCTGGCCAGCCTTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCACC 197

101

196 TCACCTTCCCTCTTCCTCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGAA 137

-------GlnAlaSerAlaSerProAspProArgProLeuArgGlu

102

CysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArgThr 154

76 TGTTGGACTGCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCAGGACC

GlnGluValThrPro 159

155 (

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CAGGAGGTTACTCCC

16

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GluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHisGly

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AAI00170 standard; DNA; 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                               Human, single exon nucleic acid probe, liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
                                                                                                                                                               Human liver single exon probe, SEQ ID No 172.
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  ВР
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2000US-0234687P.
2000US-0236359P.
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21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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ABS25182 standard; DNA; 497
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                                                                                                         (first entry)
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                                                                                                            25-FEB-2003
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Novel single exon nucleic acid probe used to measuring gene expression in
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                                                                                              Probe; human; breast disease; breast cancer; development disorder; ss; inflammatory disease; proliferative breast disease; non-carcinoma tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the prohybridises at high stringency to a nucleic acid expressed in the human
                                                                      Probe #161 used to measure gene expression in human breast sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 161; 322pp; English.
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2000US-0234687P.
2000US-0236359P.
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2000US-00608408
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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LysGluGluGluAlaProLeuLeuProArgThrHisLeuGlnAlaGluProHisGln

US-10-030-225-2_COPY_27_213 (1-187) x ABS25182 (1-497)

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497 126

Length:

Matches: Conservative: Mismatches:

4.11e-31 658.50 76.97% 76.36% 66.18%

Similarity:

Percent Similarity: Best Local Similari

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Score:

Query Match:

Indels:

Gaps:

CATGGATGCTGGACTGTCACTGAGCCAGCATGACCCCAGGAACGCCACCCTCCC 377

HisGlyCysTrpThrValThrGluProAlaAlaMetThrProGlyAsnThrThrProPro

71

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breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and noncarcinoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGGATGCTGGACTGTCACTGAGCCAGCCATGACCCCAGGCAACGCCACCCCTCCC 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGGCTCTGCCTGGCCAGCCTTTTCTGGGTCCCTGTTGGGTAAGCCCTAACCTGTCACC 197
                                                                                                                                                                                                                                                                                                                                                                                                LysGluGluGludlaProLeuLeuProArgThrHisLeuGlnAlaGluProHisGln 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's Glacese; Niemann-Pick disease; Hermansky-Pudlak syndrome; astroidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon probe from lung SEQ ID No 166,
                                                                                                                                                                       Sequence 497 BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                  Conservative:
Mismatches:
The probes are useful for predicting,
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76.36%
66.18%
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Query Match:
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pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
primary ciliary dyskinesis; pulmonary hypertension;
hyaline membrane disease.
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                                                                                                                                                                                                                 Claim 1; SEQ ID NO 166; 634pp; English.
                                                                                                                                                               Rank
                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                               Chen W,
                                                                                              26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
                                                                                                                   21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                         30-JAN-2001; 2001WO-US000665
                                                                                                                                                                             WPI; 2002-114183/15
                                            WO200186003-A2
                               Homo sapiens
                                                                                       04-FEB-2000;
                                                           15-NOV-2001
                                                                                                                                                               SG,
                                                                                                                                                                Penn
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The invention relates to a spatially-addressation in a sample derived from human lung comprising single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung cacid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12619 open reading frames derived from the 12619 open reading frames derived from the lorder are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung comprising (a) contacting the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably clabeled nucleic acids from eukaryote; lung mana, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon of expression of the exons should be assigned to a single gene; a peptide comprising one contractive should be assigned to a single gene; a peptide comprising one contractive should be assigned to a single gene; a peptide comprising one contractive should be assigned to a single gene; a peptide comprising one contractive should be assigned to a single gene; a peptide comprising one contractive microarrays having a probe with the exons, where a common pattern of the exons should be assigned to a single gene; a peptide comprising or probes/open reading frames (ORP). The probes are used for gene expre cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermanskydyskinesis, pulmonary hypertension and hyaline membrane disease. The present sequence is a single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO Pudlak syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary histiocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary ftp.wipo.int/pub/published_pct_sequences

17

BP; 81 A; 128 C; 177 G; 111 T; 0 U; 0 Other; Sequence 497

Alignment Scores:

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Claim
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                                                                                                                                                                                                                                                                               GluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHisGly 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   for gene expression analysis in human cervical cell sample.
                                                                         LysGluGluGluGluAlaProLeuLeuProArgThrHisLeuGlnAlaGluProHisGln
                                                                                     AAGGAAGAGGAGGAGCACCACTGCTCCCCAGAACCCACCTGCAGGAGGAGGCAGAGCCAAA
                                                                                                                         CATGGATGCTGGACTGTCACTGAGCCAGCCAGCCATGACCCCAGGCAACGCCACCCTCCC
                                                                                                                                                                            GAGGAGGAGGCACGACTCCCCAGAACCCACCTGCAGGCAACAACATGGA
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                                                                                                           HisGlyCysTrpThrValThrGluProAlaAlaMetThrProGlyAsnThrThrProPro
                                                                                                                                                                                                                                              cell;
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497
126
1
1
37
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                         US-10-030-225-2_COPY_27_213 (1-187) x ABS00175 (1-497)
                                          Gaps:
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26-MAY-2000; 2000US-00207456P.

30-UNN-2000; 2000US-0068408.

03-AUG-2000; 2000US-00632366.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-023459P.

04-OCT-2000; 2000GB-00024263.
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4.11e-31
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              Percent Similarity:
Best Local Similarity:
Query Match:
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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
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                                                                                                                                                                                                    The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 243 BP; 34 A; 61 C; 89 G; 59 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                   Rank DR
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(MOLE-) MOLECULAR DYNAMICS INC
                                   Chen W,
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Best Local Similarity:
Query Match:
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Human genome-derived single exon nucleic acid probes useful for analyzing
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                                                                                                                                                                                                                                                         (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                  03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                              30-JAN-2001; 2001WO-US000663
 genetic disorder; ss
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                                                        WO200157272-A2
                                                                                                                                                                      30-JUN-2000;
                             Homo sapiens
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                                                                                                                                                                                                                                                                                             The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184
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                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 12836; 639pp + Sequence Listing; English
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Matches:
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                                                                                                                                                                     Rank DR
                       04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456F.
30-UJN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-023468PP.
27-SEP-2000; 2000US-023559P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 243 BP; 34 A; 61 C;
30-JAN-2001; 2001WO-US000669
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Query Match:
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Chen W, Rank DR

Hanzel DK,

2000US-0180312P. 2000US-0207456P. 2000US-00608408.

expression in human placenta.

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183 AGAACCCACCTGCAGGCAGAGCCACACATGGATGCTGGACTGTCACTGAGCCAGCA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GluLeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThr 101
The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgThrHisteuGlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeu
                                                                                                                                  Sequence 243 BP; 34 A; 61 C; 89 G; 59 T; 0 U; 0 Other;
                                                                                                                                                                                                    243
1 1 2 0 0 0 0
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Sequence 12147, Application US/09949016
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REPREMENTE: CLOOU307
; CURRENT APLICATION NUMBER: 60/241, 755
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR PLILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREEKEQ for Windows Version 4.0
; SEQ ID NO 12147
                                                                                                                                                                                                              Sequence 4955. Applements of Applements 12348, A Sequence 12348, A Sequence 13619, A Sequence 13620, A Sequence 13621, A Sequence 13621, A Sequence 13622, A Sequence 13623, A Sequence 15644, A Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli
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Sequence 61, Appl
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US-09-949-016-16802
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LOCATION: (1)...(767677
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Query Match:
TYPE: DNA
ORGANISM: Human
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103, App
43, Appl
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Compugen Ltd.
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                          GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Match Length DB
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14.5 2824
14.5 3168
14.5 3148
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14.5 3836
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150 150 144 144 144

Result g

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Percent Similarity:
Best Local Similarity:
Query Match:
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREEEQ FOR WINGOWS VERSION 4.0
SEQ ID NO 17361
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                                                                                                                                      605023 GGACCGACCAGGCTTTCTCATAAATGCACAGCCCACGTCAGTTACACCAGCACCTACCCG 605082
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                                            7 ArgleuArgGlyProArgProGlySerLeuThrArgLeuAlaGluValSerAlaSerPro
                                                                                                                                                                                                                                    57 ValThrGluProAlaAlaMetThrProGlyAsnThrProProArg------
                                                                                                                                                                       39 LeuLeuProArgThrHisLeuGlnAlaGluProHisGlnHis-----GlyCysTrpThr
              US-10-030-225-2_COPY_27_213 (1-187) x US-09-949-016-12147 (1-767677)
                                                                                                                                                                                                                                                                                                    ---ThrProGluVal-------
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OTHER INFORMATION: n = A,T,C
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NAME/KEY: misc_feature
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US-09-949-016-17361
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Alignment Scores:

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605254 CGTCAGTTACAC---CAGCACCTACCCGGC------TCTCTTACAAACCCACAG 605298
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767677
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                        Matches:
Conservative:
Mismatches:
Indels:
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Fatent No. 6433142
GENERAL INPORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte St
NUMBER OF SEQUENCES: 143
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150.00
42.00%
32.00%
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ADDRESSEE: Genetics
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1699 GCTCCAACTÁCCCCTAAGGAGCCTGCTCCAACTÁCCCCTAAGGGGACTGCTCCAACTACC 1758
                                                                                                                                                                 154 ThrGlnGluValThrProLeuLeuLeuGluLeuGlnLysLeuProGluLeuValHisAla 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
ITILE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SUNDENIOS:
NUMBER OF GENERSS:
ADDRESSEBE: Genetics Institute, Inc.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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Matches:
Conservative:
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FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
NAME: CGERT, LUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
FELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-757-022B-83
; Sequence 83, Application US/07757022B
; Patent No. 6433142
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MEDIUM TYPE: Floppy disk
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LENGTH: 3066 base pairs
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts: U.S.A.
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Matches:
Conservative:
Mismatches:
Indels:
                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNDRER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CRET. LUADA
REGISTATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
REFERENCE/DOCKET NUMBER: 31,822
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US/07/757,022B
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INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
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Best Local Similarity:
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STRANDEDNESS:
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US-07-757-022B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                                                                                                                          ProArgleuArgGlyProArgProGlySerLeuThrArgLeuAlaGluValSerAlaSer 25
                                                                                                                                                                                                                                                                                                                       26 ProAspproArgproLeuLysGluGluGluGluAlaProLeuLeuProArgThrHisLeu 45
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                                                                                                                            US-10-030-225-2_COPY_27_213 (1-187) x US-07-757-022B-83 (1-3066)
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APPLICATION NUMBER: US/07/757,022B FILING DATE: 19910910 CLASSIFICATION: 530
Mismatches:
Indels:
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STATE: Massachusetts
COUNTRY: U.S.A.
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; Patent No. 6433142
; Patent No. 6433142
; APPLICANT: Gener, Thomas G. APPLICANT: Glark, Stephen C. APPLICANT: Turner, Katherine
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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MEDIUM TYPE: Floppy
          Local Similarity:
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US-07-757-022B-73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
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53
12
99
22
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Matches:
Conservative:
Mismatches:
Indels:
               FILING DATE: 18-JAN-1991
PRIOR PAPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
FILING DATE: 29-DEC-1989
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                      5190
                                                                                                                                                                                                                                                                                                                   NAME: CSET, LUADIN
REGISTRATION VINDER: 31,822
REFERENCE/DOCKET NUMBER: GI 51.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1017 876-5851
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 3117 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Gouble
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144.00
35.14%
28.65%
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 18-JAN-
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Best Local Similarity:
Query Match:
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US-07-757-022B-73
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TITLE OF INVENTION: Mec
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                154 ThrGlnGluValThrProLeuLeuLeuGluLeuGlnLysLeuProGluLeuValHisAla 173
                                                                                                                                                                                                                                                                                                               Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
PIPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION 1530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAA-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY AGENT: US 07/390,901
FILING DATE: 08-AUG-1889
                                                                                                                                                                                                                                                                                                                                                                    Genetics Institute, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: CBERT, LUADIN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                            Sequence 57, Application US/07757022B Patent No. 6433142 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                    87 CambridgePark Drive
                                                                                                                                                                                                                                   APPLICANT: Gesner, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Turner, Katherine APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryoc. NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                          2014 ACCACCAAGGGGCCC 2028
                                                                      174 ThrieuSerThrPro 178
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NUCLEIC ACID
DEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cambridge
STATE: Massachusetts
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Query Match:
DB:
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1963 TCTGACAGCCCGCTCCAACTACCCCTAAGGGGACTGCTCCAACTACCCCTAAGGGGCCT 2022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GlyCysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
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                                                                    6 ProArgleuArgGlyProArgProGlySerLeuThrArgleuAlaGluValSerAlaSer 25
                                                                                                                                                                                                                26 ProAspProArgProLeuLysGluGluGluGluAlaProLeuLeuProArgThrHisLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu
                                                                                                                                                                                                                                                                                                                                                                46 GlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThr ---
US-10-030-225-2_COPY_27_213 (1-187) x US-07-757-022B-57 (1-3148)
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; Patent No. 6433142
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STREET: 87 cambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-D
SOFTWARE: PatentIn Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2143 ÁCCACCAAGGGGCCC 2157
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US-10-030-225-2_COPY_27_213 (1-187) x US-07-757-022B-43 (1-3813)
                                                                                                                                                                                                                                                                                             APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hawick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge
STREET: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.25
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Matches:
Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0AN-1991
PRIOR APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1989
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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PAPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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                                                                                                                                                                                      US-07-757-022B-43
; Sequence 43, Application US/07757022B
; Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cserr, Luann
REGISTATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                             2416 ACCACCAAGGGCCC 2430
                                           174 ThrLeuSerThrPro 178
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3813 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144.00
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STRANDEDNESS: doub
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Best Local Similarity:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 ProArgleuArgGlyProArgProGlySerLeuThrArgleuAlaGluValSerAlaSer 25
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Mismatches:
Indels:
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Matches:
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION DATA: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY, AGENT INFORMATION:
NAME: CSerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELECHOME: (617)876-1170
TELECAMONICATION INFORMATION:
TELERAX: (617)876-1170
TELECAMONICATION FOR SEQ 1D NO: 103:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ 1D NO: 103:
LENGRATION FOR SEQ 1D NO: 103:
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LENGRATION FOR SEQ 1D NO: 103
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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144.00
35.14%
28.65%
14.47%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                         1502 CCACCCTGAGAAGCCGGCACCCACCACCTGAG-GAGCTCGCACCACCACCACCTGAG 1560
                                                                                            1561 ---GAGCCCACACCCACCACCTGAGAGCCTGCTCCCACCACCCCAAGGCAGCGGCT 1617
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6 ProArgleuArgGlyProArgProGlySerLeuThrArgLeuAlaGluValSerAlaSer 25
                                                                  26 ProAspProArgProLeuLysGluGluGluGluAlaProLeuLeuProArgThrHisLeu 45
                                                                                                                                                                                                          65 -----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu 82
                                                                                                                                       46 GlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThr---
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Patent No. 6433142
GENERAL INFORMATION:
APPLICANT: Gener, Thomas G.
APPLICANT: Turner, Ketherine
APPLICANT: Turner, Katherine
APPLICANT: Hewlack, Rodney M.
TITLE AND THE APPLICANT: Turner, Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
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CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
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1684 ---GAGCCCACACCACCACCCTGAGGAGCCTGCTCCCACCACTCCCAAGGCAGGGCGCT 1740
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12
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22
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGEN: INFORMATION:
'NAMB: CSETY, LUADN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
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                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 3936 base pairs
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144.00
35.14%
28.65%
14.47%
                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3936 base pai
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
US-07-757-022B-41
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2023 GCTCCAACTACCCCTAAGGAGCCTGCTCCAACTACCCCTAAGGGGACTGCTCCAACTACC 2082
                                         1690 ---GAGCCCACCACCACCACCCCTGAGGAGCCTGCTCCCACCACTCCCAAGGCAGCGGGT 1746
                                                                                                                      1903 AAGAAGCCTGCCCCAAGGAGCTTGCACCCACCACCACCAAGGAGCCCACATCCACCACC 1962
                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                                                                                                                                                                                                                                                                       114 GluGluGluGluHlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 GlyCysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 ThrGlnGluValThrProLeuLeuLeuGluLeuGlnLysLeuProGluLeuValHisAla 173
    26 ProAspProArgProLeuLysGluGluGluGluAlaProLeuLeuProArgThrHisLeu 45
                                                                                                                                                                      46 GlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThr---
                                                                                                                                                                                                             1807 AAGGAGCCTGCTCCAACTACCCCTAAGGAGACTGCTCCAACTACCCCT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/07757022B
| Sequence 49, Application US/07757022B
| Patent NO. 6433142
| GENERAL INFORMATION:
| APPLICANT: Gener, Thomas G. APPLICANT: Clark, Stephen C. APPLICANT: Hewick, Rodney M. TITLE OF INVENTION: Megakaryocyte Stimulating Factors NUMBER OF SEQUENCES: 143
| CORRESPONDENCE ADDRESS: CORRESPER: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: Genetics Institute,
87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2143 ACCACCAAGGGGCCC 2157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 ThrLeuSerThrPro 178
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STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
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                                                                              APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/757,0228 FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
CLASSIFICATION DATA:
APPLICATION NUMBER: 05 07/643,502
FILING DATE: 18-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
PRIOR APPLICATION NUMBER: US 07/57,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
PRIOR APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1889
ATTORNEY AGENT: INFORMATION:
NUMBER: US 07/390,901
FILING DATE: 18-DEC-1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: CBETT, LUADIN
REGISTRATION NUMBER: 31,822
REGISTRATION NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
                                                                          Sequence 141, Application US/07757022B
Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 3942 base pairs
2137 ACCACCAAGGGCCC 2151
                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
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35.14%
28.65%
14.47%
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CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
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                                           RESULT 10
US-07-757-022B-141
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Pred. No.:
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                 STATE:
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OB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCAACACCCCTAAGGAGCCTGCTCCAACTACCCCTAAGGAGCCTGCTCCAACTACCCCT 1809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1906 AAGAAGCCTGCCCCCAAGGAGCTTGCACCCACCACCACCAAGGAGCCCACATCCACCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 GlyCysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
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Indels:
                                               ATTORNEY/AGENT INFOLDANT
NAME: CSGTY, LOADN
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GE 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPHONE: (617)876-1170
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 3945 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
RILING DATE: 08-AUG-1989
ATTORNEY AGENT INFORMATION:
NAME: CSETI, LUANN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCACCAAGGGGCCC 2160
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Query Match:
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LOCATION:
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RESULT 12

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6 ProArgleuArgGlyProArgProGlySerLeuThrArgleuAlaGluValSerAlaSer 25
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                                                        APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3963
53
12
99
22
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-7AM-1991
PRIOR APPLICATION NUMBER: US 07/546,114
PRIOR APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
PRIOR APPLICATION NUMBER: US 07/457,196
FILING DATE: 08-AUG-1889
FILING DATE: 08-AUG-1889
FILING DATE: 08-AUG-1889
FILING DATE: 08-AUG-1889
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                E: Genetics Institute, Inc. 87 CambridgePark Drive
Sequence 45, Application US/07757022B Patent No. 6433142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: CBerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0144
144.00
35.148
28.658
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                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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CITY: Cambridge
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Best Local Similarity:
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ATTORNEY/AGENT INFORMATION:
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1711 ---GAGCCCACACCCACCCCCTGAGGAGCCTGCTCCCACTCCCAAGGCAGGGGGCT 1767
                                                                    1768 CCCAACACCCCTAAGGAGCCTGCTCCAACTACCCCTAAGGAGCCTGCTCCAACTACCCCT 1827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrGlnGluValThrProLeuLeuGluLeuGlnLysLeuProGluLeuValHisAla 173
                                                                                                       -----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu 82
                                 46 GlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThr--- 64
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                                                                                                                                        1828 AAGGAGCCTGCTCCAÁCTACCCCTAAGGAGACTGCTCCAACTACCCCT---
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APPLICANT: Gener, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
CLASSIFICATION: 530
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PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/457,196
FILING DATE: 29-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
~weither: IBM PC compatible
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STATE: Massachusetts
COUNTRY: U.S.A.
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CITY: Ca
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Patent No. 6433142
NAME: CBELT, LUBIN
REGIGTRATION UNDBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                        31,822
ER: GI
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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; LOCATION:
US-07-757-022B-59
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US-07-757-022B-47
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2086 TCTGACAGCCCGCTCCAACTACCCCTAAGGGGACTGCTCCAACTACCCCTAAGGAGCCT 2145
       1870 cccaacaccccraaggagccrgcrccaacracccraaggagccrgcrccaacracccr 1929
                                                                                                                                                                                         ------AAAGGGACTGCTCCAACTACCCTCAAGGAACTGCACCCACTACTCCC 2025
                                                                                                                                                                                                                                                                                  2026 AAGAAGCCTGCCCCCAAGGAGCTTGCACCCACCACCAAGGAGCCCACCATCCACCACC 2085
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                                                                                                                                                                                                                                       114 GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
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                                                     -----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu 82
                                                                                                1930 AAGGAGCCTGCTCCAACTACCCCTAAGGAGACTGCTCCAACTACCCCT-----
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PRIOR APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/643,502
PRIOR APPLICATION NUMBER: US 07/546,114
PLING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/546,114
PLING DATE: 29-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/57,196
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,901
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APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
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FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/07757022B
Patent No. 6433142
GENERAL INFORMATION:
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87 CambridgePark Drive
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APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Hewick, Rodney M.
TITLE OF INVENTION: Megakaryoc;
UNDHER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institut.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 31,822
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SOFTWARE: Patentl
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CITY: Cambridge
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APPLICANT: Gesner, Thomas G.
APPLICANT: Clark, Stephen C.
APPLICANT: Turner, Katherine
APPLICANT: Turner, Katherine
APPLICANT: Turner, Rodney M.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-UAN-1991
PRICE APPLICATION NATA:
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
PRICE APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 29-DEC-1989
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AGG-1989
ATTORNEY/AGENT INFORMATION:
NAME: CREET, LUMBIN
                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,022B
FILING DATE: 19910910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOWNS: unknown
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35.14%
28.65%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STATE: Massachusetts
COUNTRY: U.S.A.
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Best Local Similarity:
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US-07-757-022B-47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 GlyCysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 ThrGlnGluValThrProLeuLeuLeuGluLeuGlnLysLeuProGluLeuValHisAla 173
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                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
Indels:
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
TELEPAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 4086 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
FEATURE: TOPOLOGY:
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, LOCATION: 1..4083
US-07-757-022B-39
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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Search completed: February 22, 2005, 03:20:11 Job time: 464 secs

Scoring table:

Perfect score:

Seguence:

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Run on:

Minimum DB seq Maximum DB seq

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APPLICANT: Rent, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Banzel, David R.
APPLICANT: Banzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
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Sequence 7595, Ap
Sequence 382, App
Sequence 88274, A
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Sequence 94182, A
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Sequence 1421, Ap
Sequence 36853, A
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                                                                                        Sequence 156, App
Sequence 16984, A
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Sequence 1,
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Sequence 8
Sequence 7
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US-09-764-891-7594
US-09-764-891-7595
US-10-087-192-382
US-10-437-963-88274
US-10-322-281-700
US-10-108-260A-1421
US-10-363-345A-36853
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) US-09-976-059-1
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Patent No. US20020048763A1
GENERAL INFORMATION:
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31422 1
9025608
                                Length
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75853
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     Query
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                                Score
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Result
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1. (cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

1. (cgn2_6/ptodata/2/pubpna/DSO6_PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

1. (cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5384158 segs, 2955248155 residues
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Maximum Match 100%
Libting first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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length: 2000000000
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Database

Appli Appli Appli

3, Appli 47999, A

1, Appli 1, Appli 2, Appli 2, Appli 14, Appli 89, Appli 90, Appl

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GluGluValThrPro 159
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PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-10-3
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
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ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: OLEK, ALexander
APPLICANT: OLEK, ALExander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: Display Kurt
FILLE OF INVENTION: Display of Diseases Associated with Cell Cycle
FILE REFERENCE: 5013.1004
CURRENT APPLICATION NUMBER: US/10/221,613
CURRENT APPLICATION NUMBER: PCT/EP01/02945
DE 10013847.00
DE 10019173.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
                                                                                                                                                              N: EXPRESSED IN BT474, SIGNAL = 0.85

N: EXPRESSED IN BONE MARROW, SIGNAL = 0.92

N: EXPRESSED IN HELLOO, SIGNAL = 0.92

N: EXPRESSED IN FETAL LIVER, SIGNAL = 0.75

N: EXPRESSED IN LUNG, SIGNAL = 0.92

N: EXPRESSED IN LUNG, SIGNAL = 0.96

N: EXPRESSED IN BADILT LIVER, SIGNAL = 0.96

N: EXPRESSED IN HELA, SIGNAL = 1.4

N: EXPRESSED IN HELA, SIGNAL = 1.4

N: EXPRESSED IN HERAT, SIGNAL = 1.4

N: MT HIT: AFILIISR 2, EVALUE 1.50e+00

N: WISSPROT HIT: P31157, EVALUE 1.50e+10
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16984
LENGTH: 243
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Matches:
Conservative:
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2000-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430.00
98.77%
97.53%
43.22%
                                                                        TYPE: DNA ORGANISM: Homo sapiens
                                                                                                       FEATURE:
OTHER INFORMATION: MOTHER INFORMATION: E
OTHER INFORMATION: E
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OTHER INFORMATION:
US-09-864-761-16984
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Query Match:
DB:
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; Publication No. US20
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                US-10-030-225-2_COPY_27_213 (1-187) x US-10-221-613-274 (1-6694)
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Matches:
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                                                                                             TYPE: DNA ORGANISM: Artificial Sequence
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149.50
41.92$
26.26$
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
2000-06-30
2000-09-01
NUMBER OF SEQ ID NOS: 428
SEQ ID NO 274
LENGTH: 6694
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Best Local Similarity:
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        TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21 (53313) B CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 73128
SEQ ID NO 14755
LENGTH: 1602
                                                                                                                                                                                                                                                                                                                     CCCCTCTCCTCTTCACCATCGCCTCCGTCCTCTCCTTCGTCGCCTCCACGCGCCCCT 230
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Matches:
Conservative:
Mismatches:
                                                                                                                                            OTHER INFORMATION: Clone ID: LIB3039-011-B5 FLI
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US-10-424-599-22752
; Sequence 22752, Application US/10424599
; Publication No. US20040031072A1
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149.00
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Best Local Similarity:
Query Match:
DB:
                                                                                                         TYPE: DNA
ORGANISM: Glycine
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Solu Yihua
APPLICANT: Zhou Yihua
APPLICANT: Can Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 22752
LENGTH: 1782
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US-10-424-599-22752
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Glycine
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Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-030-225-2_COPY_27_213 (1-187) x US-10-124-557-13 (1-2824)
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                               171 ValHisAlaThrLeuSer-----ThrProAsnProAspAsn
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Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/546,116
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/57,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE DESCRIPTION: SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    ; Sequence 13, Application US/10124557; Publication No. US20020137894A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2824 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 13:
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STRANDEDNESS: double
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COMPUTER READABLE FORM:
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                                                                  PUBLICATION NO. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: PCT/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2275 CCCCGTCCACCTACAAAACCAAA------ACCCAATCCCCAACCCTCC 2228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2176 TCCAAATCTCCAACTCCTCCTCCAAACCCAAAAATCCAAACCCCA-----ACCATT 2123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GlnAlaSerAlaSerProAspProArgProLeu-----ArgGluGluGluBluAla 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 ArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHisGlyCysTrpThrVal 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProArgProGlySerLeuThrArgLeuAlaGluValSerAlaSerProAspProArgPro 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 HisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThrProGlyAsnThrThr 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----ThrProLeuArgleu 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-030-225-2_COPY_27_213 (1-187) x US-10-311-455-979 (1-6456)
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Matches:
Conservative:
Mismatches:
Indels:
                                                 Sequence 979, Application US/10311455
Publication No. US20030143606A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
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147.00
42.56%
29.23%
14.77%
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SEQ ID NO 979
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Best Local Similarity:
RESULT 6
US-10-311-455-979/c
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29-DEC-1989

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FILING DATE:
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                                                                                                                                   1579 AAGAAGCCTGCCCCAAGGAGCTTGCACCCACCACCACGAGGAGCCCACATCCACCACC 1638
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                                                                                                                                                                                                                                        83 LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                                                                                                                                                                                                                                     -----AspProArgProLeuArg 113
                                                                                                                                                                                                                                                                                                                                                                 GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 ThrGlnGluValThrProLeuLeuLeuGluLeuGlnLysLeuProGluLeuValHisAla 173
                                               26 ProAspProArgProLeuLysGluGluGluGluAlaProLeuLeuProArgThrHisLeu 45
                                                                                                              64
                                                                                                                                                                         65 -----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu 82
                                                                             1366 --- GAGCCCACACCACCACCCTGAGGAGCCTGCTCCCACCACTCCCAAGGCAGGGCT
                                                                                                            GlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 83, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
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COMPUTER: IBM PC compatible
DERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
SNT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-2NA-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INV...
NUMBER OF SEQUENCES: ...
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, In
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                        103 AlaSerAlaSerPro----
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1726 AAGGAGCCTGCCAACTACCCCTAAGGAGACTGCTCCAACTACCCCT------ 1773
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Matches:
Conservative:
Mismatches:
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                     NAME: Cserr, Luann
REGISTARION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
RELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-5170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
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SEQUENCE DESCRIPTION: SEQ ID
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144.00
35.14%
28.65%
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Best Local Similarity:
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1774 AAGAAGCCTGCCCCCAAGGAGCTTGCACCACCACCACCAAGGAGCCCACATCCACCACC 1833
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                                                                                          1618 CCCAACACCCCTAAGGAGCCTGCTCCAACTACCCCTAAGGAGCCTGCTCCAACTACCCCT 1677
                                                                                                                                                                                                                                        83 LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                                                                                                                                                                                                                                                                     -----AspProArgProLeuArg 113
                                                                                                                                                                                                                                                                                                                                                                                                                                  114 GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
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                                                                                                                                         -----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu 82
                                             GlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluProAlaAlaMetThr ---
                                                                                                                                                                                    1678 AAGGAGCCTGCTCCAACTACCCCTAAGGAGACTGCTCCAACTACCCCT-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.25
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COMPUTER: IBM PC compatible
COMPAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
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APPLICANT: Turner, Katherine; Jacobs, Kenneth; Hewick, Rodney M. Gesner, Thomas G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07 FILING DATE: 08-AUG-1989
NEV AGENT TATAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                   103 AlaSerAlaSerPro-
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                                                                                                                                    Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-030-225-2_COPY_27_213 (1-187) x US-10-124-557-73 (1-3117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
CORPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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Mismatches:
Indels:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-0A-01991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
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Matches:
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FILING DATE: 16-Apr-2002
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REGISTRATION UNMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1.3114
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: <Unknown>
                                        Sequence 73, Application US/10124557
Publication No. US20020137894A1
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                                                                                  GENERAL INFORMATION:
APPLICANT: Turner, Katherine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3117 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                         CITY: Cambridge
STATE: Massachusetts
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COMPUTER READABLE FORM:
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35.14%
28.65%
14.47%
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Query Match:
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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 GluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134 GlyCysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
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53
12
99
22
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Conservative:
Mismatches:
                     5190
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                                                                                                                                                                                                                                             LOCATION: 1.3147
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3148 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Publication No. US20020137894A1
GENERAL INFORMATION:
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144.00
35.14%
28.65%
14.47%
                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: cDNA PEATURE:
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                                                                                                                                                                                                                              NAME/KEY:
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-124-557-103
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1963 ---GAGCCCACACCCACCACCTGGGAGCCTGCTCCCACCACTCCCAAGGCAGCGGCT 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ProArgieuArgGlyProArgProGlySerLeuThrArgieuAlaGluValSerAlaSer
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APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Genner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-UN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
APPLICATION NUMBER: US 07/390,901
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                    Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <UNKNOWN>
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US-10-124-557-103
                                                                                                                                                                                ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                     ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
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SEQUENCE CHARACTERISTICS:
LENGTH: 3420 base pai
                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                 NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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STRANDEDNESS: doubl
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Best Local Similarity:
Query Match:
DB:
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Matches:
Conservative:
Mismatches:
Indels:
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SEQUENCE DESCRIPTION: SEQ ID NO: 43:
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publication No. US2002013/894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 3813 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Jacobs, Kenneth
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Gesner, Thomas G.
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Best Local Similarity:
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No.:
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                                                                                                                                                                         LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                                                                                                                                                                                                                                           GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
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|TCTGACAAGCCGGCTCCAACTACCCCTAAGGGGACTGCTCCAACTACCCCTAAGGAGCCT
                                      ----ProGlyAsnThrThrProProArgThrProGluValThrProLeuArgLeuGlu
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Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
CORRESPONDENCE ADDRESS:
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COMPUTER: 1BM PC Compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
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APPLICATION NUMBER: US 07/457,196
APPLICATION ES-29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
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APPLICATION NUMBER: US/10/124,557
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REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: <Unknown>
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Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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COMPUTER READABLE FORM:
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  83 LeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAspThrGln 102
                                                                                              ---AspProArgProLeuArg 113
                                                                                                                                                                                     114 GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
                                                                                                                                                                                                                                                                                    134 GlyCysTrpThrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
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COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/454,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DGC-1989

"APPLICATION NUMBER: US 07/390,901
FILING DATE: 28-DBC-1989

"APPLICATION NUMBER: US 07/390,901
FILING DATE: 18-AMG-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 141, Application US/10124557
Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI 5190
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STREET: 87 CambridgePark Drive
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REGISTRATION NUMBER: 31,822
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)876-1170
                                                                                                103 AlaSerAlaSerPro-----
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STRANDEDNESS: double
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STATE: Massachusetts
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                           COUNTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER: IDAPY disk
COMPUTER: IDAPY SYTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: CURROWN>
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TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1889
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
ATTORNEY/AGENT INFORMATION:
                                                                      ADDRESSEE: Genetics Institute, Inc
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 41:
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TELEFAX: (617)876-5851
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SEQUENCE CHARACTERISTICS:
LENGTH: 3936 base pairs
                                                                                                                      CITY: Cambridge
STATE: Massachusetts
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STRANDEDNESS: double
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Best Local Similarity:
Query Match:
DB:
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Percent Similarity:
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DB:
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Jacobs, Kenneth
Hewick, Rodney M.
Gesner, Thomas G.
OF INVENTION: Megakaryocyte Stimulating Factors
R OF SEQUENCES: 143
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Matches:
Conservative:
Mismatches:
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STREET: 87 CambridgePark Drive
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                                                              LOCATION: 1..3939
SEQUENCE DESCRIPTION: SEQ ID NO: 141:
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Publication No. US20020137894A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
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                                                                                                                                              0.000452
TOPOLOGY: unknown MOLECULE TYPE: cDNA
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                                               NAME/KEY:
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Best Local Similarity:
Query Match:
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                                                                                              US-10-124-557-141
                                                                                                                              Alignment Scores:
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|1750 CCCAACACCCCTAAGGAGCCTGCTCCAACTACCCCTAAGGAGCCTGCTCCAACTACCCCT 1809
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Matches:
Conservative:
Mismatches:
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APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1.3942
SEQUENCE DESCRIPTION: SEQ ID NO: 49:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 3945 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
STATE: Massachusetts
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STRANDEDNESS: double
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28.65%
14.47%
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2026 GCTCCAACTACCCCTAAGGAGCCTGCTCCAACTACCCCTAAGGGGAACTGCTCCAACTACC 2085
                                                                                                                                                                                                                2086 CTCAAGGAACCTGCACCACTACTCCCAAGAAGCCTGCCCCAAGGAGCTTGCACCAACC 2145
1906 AAGAAGCCTGCCCCCAAGGAGCTTGCACCACCACCACCACAAGGAGCCCACATCCACCACC 1965
                                                                          1966 TCTGACAAGCCGCTCCAACTACCCCTAAGGGACTGCTCCAACTACCCCTAAGGAGCT 2025
                                                                                                                    134 GlyCysTrpinrValThrGluProAlaAlaLeuThrProGlyAsnAlaThrProProArg 153
                                                                                                                                                                                        154 ThrGlnGluValThrProLeuLeuCluLeuGlnLysLeuProGluLeuValHisAla 173
                                                 114 GluGluGluGluAlaArgLeuLeuProArgThrHisLeuGlnAlaGluLeuHisGlnHis 133
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 07-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAJJOLES
BX336289 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
CLIONE CSODIO27YA01 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (200 pt. 1 (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) (200 pt. 1) 
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                  BX381620
BX337466
BX3373151
BX3562106
BX336623
BX3379676
BX3379676
BX3370177
BX336023
BX336023
BX358070
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/organism="Homo sapiens"
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Homo sapiens
RESULT 1
BX336289
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlp
-MODEL=frame+ p2n.model -DEV=xlp
-Genz_1/USPTO_spool_p/US10030225/runat_18022005_100355_2354/app_query.fasta_1.327
-B=FGT_2/CSPTZ_1/USPTO_spool_p/US10030225/runat_18022005_100355_2354/app_query.fasta_1.327
-DESET_CPMT=fastap -SUFFTX=rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -THR MAX=100 -THR MINO -ALIGN=15 -MODE=LOCAL
-OUTHFWT=ptc -NORM=ext -HEAFSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER=US10030225_@CGN 1 1_5180 @runat_18022005_100355_2354 -NCPU=6 -ICPU=3
-NO_WMAP -LARREQUERY -NEG_SCORES=0 -WAIT -DSPBILOK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDF=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPE -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX387234 BX387234
BX365974 BX365974
BX365998 BX365998
BX345999 BX346975
BX34509 BX34609
BX34809 BX34508
                                                                                                                  February 22, 2005, 01:12:02; Search time 3107 Seconds (without alignments) 2290.962 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX336289 BX336289
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995
1 LPVKKPRLRGPRPGSLTRLA.....PELVHATLSTPNPDNQVTIK 187
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           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                 OM protein - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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DB:
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            AUTHORS
TITLE
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                    /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                                                                                                                                                                                     CTCCCCGTGAAGAAGCCGCGGCTCCGCGGACCACGGCCTGGGAGCCTCACGAGGCTCGCA
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clone CS0DI034YP24 5-PRIME, mRNA sequence.
BX387234
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Matches:
Conservative:
Mismatches:
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                          /clone="CS0DI027YA01"
             xref="taxon:9606"
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Genosoppe - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: sequencope.cns.fr. Web : www.genosoppe.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSFORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites.of the pCMVSPORT 6 vector. Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                            There is a virtual cDNA representing this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?s=CS5AA014ZD04RM1&c=7348.r. Location/Qualifiers
                                                                              On May 8, 2003 this sequence version replaced gi:30447511 Contact: Genoscope
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1186
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Pull-length cDNA libraries and normalization Unpublished (2001)
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/clone="CSODI034YP24"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

12 (bases 1 to 867)

13 (bases 1 to 867)

14 (bases 1 to 867)

15 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

16 Pull-length cDNA libraries and normalization

17 Mupublished (2001)

18 On May 13, 2003 this sequence version replaced gi:30615118.

19 Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 ENRY cedex - FRANCE

Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr

18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX403263 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
CLONE CS0DI075YH10 5-PRIME, mRNA sequence.
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207 CCCAGAACCCACCTGCAGGCAGAGCCACACCCAACATGCTGGATGCTGGACTGTCACTGAGCCA 266
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                       447 CTCCCCAGAACCCACCTGCAGGCAGAGCTACACACATGGATGTTGGACTGTCACTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        507 CCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCCCAGGACCCAGGAGGTTACTCCCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           567 CTGCTGGAGCTGCAGAAGCTGCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT
                                                                                                                                                  81 LeuGluLeuGlnLysLeuProGlyLeuAlaSerThrLeuSerThrProAsnProAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope Control of Sequencage Genoscope - Centre National de Sequencage Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                         BX365974 BX365974 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI031YB04 5-PRIME, mRNA sequence.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.'
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1 (Dases 1 to 866)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length CDNA libraries and normalization
Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30370960.
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                                                                  563 CIGCIGGAGCIGCAGAAGCIGCCAGAAIIGGICCACGCAACCIIGAGIACCCCIAACCCI
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                                                                                                                                                  623 GATAACCAGGTGACCATCAAG 643
                                                                                                                    181 AspAsnGlnValThrileLys 187
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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             Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                            x BX403263 (1-867)
                                                                                                        Gaps:
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                                                                                                                                            US-10-030-225-2_COPY_27_213 (1-187)
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BX365998.2 GI:46306893
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SOURCE
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             Pred. No.:
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digested with Not I and cloned
                                                                                                       There is a virtual cDNA representing this cluster. For more information about this cluster and the virtual cDNA, see http://www.genoscope.cns.fr/cdna?e=CS2BAX14ZD10_AX24ZB5_1&c=7348.r.iocation/Qualifiers
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                    into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7348.r
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                                                                                                                                                                                                              /organism="Homo sapiens"
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/ clone="Ist strand cDNA was primed with a NotI-oligo (GT)
// note="Ist strand cDNA was primed with a NotI-oligo (GT)
// prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AlaAlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArg
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Mismatches:
Indels:
Gaps:
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  enriched, double-strand cDNA was
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992.00
100.00%
99.47%
99.70%
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140 510 630

180

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On May 2, 2003 this sequence version replaced gi:30336333.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX345009 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI060YF04 5-PRIME, mRNA sequence.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Pith prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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                                            451 CICCCCAGAACCCACCIGCAGGCAGAGCIACACCCAACAIGGAIGTIGGACIGICACIGAG
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      ThrGlnAlaSerAlaSerProAspProArgProLeuArgGluGluGluAlaArgLeu
                                                                                                                        LeuProArgThrHisLeuGlnAlaGluLeuHisGlnHisGlyCysTrpThrValThrGlu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 881)
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqret@genoscope.cns.fr, Web : www.seorope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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BX344975
BX344975 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI005YP06 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 872)
Li, W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization (Dmbb)ished (2001)
On May 2, 2003 this sequence version replaced gi:30346327.
Contact: Genoscope
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Mismatches:
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/db_xref="taxon:9606"
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Best Local Similarity:
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db treef="taxon:866"
/clone="CSODIO51YH09"
/clone="CSODIO51YH09"
/clone lib="PlaceENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PlaceTNTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Library was normalized."
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BX398022 GI:46876522
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                                                                                                                                                                                                                                                                                                                                                                                                                                       452 CTCCCCAGAACCCACCTGCAGGCAGAGCTACACCAACATGGATGTTGGACTGTCACTGAG
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                                                  GluValSerAlaSerProAspProArgProLeuLysGluGluGluGluAlaProLeuLeu
                                                                                                               AlaAlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArg
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Catarrhini; Hominidae;
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Mammalia, Butheria, Primates, Catarrhini, Hon
1 (bases 1 to 900)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Vall-length cDNA libraries and normalization
Unpublished (2001)
(1-187) x BX345009 (1-881)
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Homo sapiens (human)
Homo sapiens
 US-10-030-225-2_COPY_27_213
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BX334584 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSOD1004YJ21 5-PRIME, mRNA sequence.
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                                                                                                                                             LeuproVallysLysProArgLeuArgGlyProArgProGlySerLeuThrArgLeuAla
                                                                                                                                                                                                                                                                         ProArgThrHisLeuGlnAlaGluProHisGlnHisGlyCysTrpThrValThrGluPro
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Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                               US-10-030-225-2_COPY_27_213 (1-187) x BX398022 (1-900)
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630

570

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                      635 Dp mRNA linear EST 23-APR-2004
BX357282 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
GLONE CSODI023YN23 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 936)

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/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
      571 CTGCTGGAGCTGCAGAAGCTGCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCT
                                                                                                           LeuLeuGluLeuGlnLysLeuProGluLeuValHisAlaThrLeuSerThrProAsnPro
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 917)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector, Library was normalized.
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                                                                                                                                                                                                 On May 1, 2003 this sequence version replaced gi:30310346.
Contact: Genoscope
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BX397246
938 bp. mRNA linear EST 28-APR-2004
8X397246 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CLONE CSDDI032YI06 5-PRIME, mRNA sequence.
BX397246
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1 (bases 1 to 938)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Evil-length cDNA libraries and normalization
Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30613343.

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Contact: Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  391 ACCCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGAAGGAGGAGGCACGACTG
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Mismatches:
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1 (base 1 to 936)

1 (base 1 to 936)

1 (base 2 to 936)

2 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

1 Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30443700.

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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX381620 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODIO68YE01 5-PRIME, mRNA sequence.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
CCCAGAACCCACGCAGAGCCACACACCAAGGATGCTGGACTGTCACTGAGCCA
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                                                                                      AlaAlaMetThrProGlyAsnThrThrProProArgThrProGluValThrProLeuArg
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1068YE01"
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FEATURES

COMMENT

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Homo sapiens
Homo sapiens
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/tlone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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Genoscope - Centrer National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Bmail: seqret@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMYSPORT & vector. Library
was normalized, Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ScoR V
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Fupublished (2001)
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947 bp mRNA
X359737 Homo sapiens PLACENTA COT 25-NORM
lone CSODI060YF04 5-PRIME, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1060YF04"
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1 (base 1 to 960)

2 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

1 mpublished (2001)

On May 8, 2003 this sequence version replaced gi:30452951.

Contact: Genoscope

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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECRR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                      BX381477

BX381477 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO66YK17 5-PRIME, mRNA sequence.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, couble-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                     LeuProArgThrHisLeuGlnAlaGluLeuHisGlnHisGlyCysTrpThrValThrGlu
                             CTCCCCAGAACCCACCTGCAGGCAGAGCTACACCAACATGGATGTTGGACTGTCACTGAG
           ThrGlnAlaSerAlaSerProAspProArgProLeuArgGluGluGluGluAlaArgLeu
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea 1 to 967)

2 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

L Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30374142.

Contact: Genoscope

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Email: segre@Genoscope.cns.fr. Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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BX357315 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA clone CSODI024YG21 5-PRIME, mRNA sequence.
BX357315
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LeuGluLeuGlnLysLeuProGlyLeuAlaSerThrThrLeuSerThrProAsnProAsp 100
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Matches:
Conservative:
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MYDHIDQDVDSCEKWINCKSDFLIKYLSQWLRDLPSCPCAYPLEAMDSPVSLQDEHQG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Secretory protein or membrane protein
Patent: E105182-A 153 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and
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Key Location/Qualifiers
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Pred. No. 6.5e-129;
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/organism="Homo sapiens"
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JP 2002017376-A/77.
Homo sapiens (human)
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1 (bases 1 to 2981)

Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Yoshida,K. and Masuho,Y. Differentiation growth factor
Patent: WO 0104312-A 1 18-JAN-2001;
HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA, YURI KAWAI,KENJI SOSHIDA,YASUHIKO MASUHO
SHOMO Sapiens (human)
PN WO 0104312-A/1
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                             OS Homo sapiens (human)
PN WO 0104312-A/1
PD 18-JAN-2001
PP 06-JUL-2000 WO 2000JP004514
PR 08-JUL-1999 JP 99P 194179,18-OCT-1999 US 60/159586 F
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Unpublished
2 (bases 1 to 2981)
Isogai, T. and Yamamoto, J.
Direct Submission
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                                                                                               07-JUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
                                                      OS Homo sapiens (human)
PN JP 200201376-A/77
PN JP 200201376-A/77
PN JP 200201376-A/77
PN JP 200201376-A/77
PN JP 200201376-A/77
PN JP 1 TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASI
PN SUGIYAMA,
PN KOJI HAYASHI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/
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Secretory protein or membrane protein
FH Key Location/Qualifiers
FT CDS (58). (1770).
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100.0%; Pred. No. 6.5e-129;
ive 0; Mismatches 0;
Hayashi,K.
Secretory protein or membrane protein
Patent: JP 2002017376-A 77 22-JAN-2002;
HELIX RESEARCH INSTITUTE
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    .2981
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    /db_xref="taxon:9606"

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Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) HRI human cDNA sequencing project; cDNA 5'- & 3'-end one pass sequencing, clone selection and full insert sequencing: Helix Research Institute (supported by Japan Key Technology Center etc.); cDNA library construction: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center. /translation="mralingragillcvlllaalleraalglevkkprlikgprpgsltr laevsaspdprplkeeeerapllprthloaephohogcwtvtepaamtggntpprtpev typlkelogkthglasttlerprdygsaspdpprplerebrallprthloaelhohog cwtvtepaalfpgntprtprtogvyfplilelogklpelvhatistpnddygvtikvvedp oaevsidllaepsnpppoptlswlpainpprtmopytrylik SEDIEGEDOEDKEEDEEGALWFNGTTDNWDGGWLAPCDWVFCDSVSYDYEPQKEWSP WSPCSGNCSTGKQQRTRPCGYGCTATETRTCDLPSCPGTEDKDTLGLPSEBWILLARN ATDWHDQDVDSCEKWINCKSDFLIKYLSQWLRDLPSCPCAYPLEAMDSPVSLQDEHQG RSFWRDASGPRERLDIYQPTARFCLRSWLSGESSTLAAQHCCYDEDSRLLTRGKGAG MPNLISTDFSPKLHFKFDTTPWILCKGDWSRLHAVLPPNNGRACTDNPLEEEYLAQLQ EAKEY" PRI 03-SEP-2002 117 61 CTGGAGGGGGCTAGGGCTCCCCGTGAAGAAGCCGCGGGCGCGCACCACGGCCTGGG 120 CTGGAGGCGCCCTAGGGCTCCCCGTGAAGAGCCGCGGCGCTCCGCGGGACCACGGCCTGGG 177 180 181 GAGGAGGCACCACACTCCCCAGAACCCACCTGCAGGCAGAGCCACACCAACATGGATGC 240 9 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Ota, T., Nishikawa, T., Suzuki, Y., Kawai-Hio, Y., Hayashi, K., Ishii, S., Saito, K., Yamamoto, J., Wakamatsu, A., Nagai, T., Nakamura, Y., Nagahari, K., Sugano, S. and Isogai, T. HRI human cDNA sequencing project ö 100.0%; Score 639; DB 9; Length 2981; ilarity 100.0%; Pred. No. 6.5e-129; Conservative 0; Mismatches 0; Indels 0 AK075445
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SED IS GEORGEBERGALWFNGTTDNWDGWLAPGDWYFKDSVSYDYEPQKEWSP
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Pred. No. 3.2e-128;
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114..1748
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/gene="TAIL1"
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Rossi, V.
Direct Submission
Submitted (16-SEP-2003) Rossi V., Department of Biology, University of Padua, viale G. Colombo, 3 - Padova, 35131, ITALY
Location/Qualifiers
1. .2883
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/codon start=1
/product="thrombospondin and AMOP containing isthmin-like
1 protein, (Tail1)"
                                                                                     357
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rossi, V., Beffagna, G., Rampazzo, A., Bauce, B. and Danieli, G.A. TAIL1: an isthmin-like gene, containing type 1 thrombospondin-repeat and AMOP domain, mapped to ARVDI critical
AGTACCCCTAACCCTGATACCCAGGCTTCAGCCTCCCCAGATCCTAGGCCTCTGAGGGAAA
                                                                                                                                                                                                                                                                             GAGGAGGAGGCACGACTCCCCCAGAACCCACCTGCAGGCGAGACCTACACCACATGGA
                                                                                                                     GAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCACAACCTTG
                                                                                                                                               GAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAGCAGCACCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens mRNA for Tail1 protein.
AJ583024.1 GI:48958174
AJ583024.1 Tail1 protein; thrombospondin and AMOP (isthmin-like 1 protein; thrombospondin and AMOP (Homo sapiens (human))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
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'dev_stage="adult"
'. .2883
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36. .1751
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PAT 18-SEP-2002

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 750)
Ota, T., Isogai, T., Nishikawa, T., Kawai, Y., Sugiyama, T. and Hayashi, K.
                                                                                                                                                                                                                                     Homo sapiens (human)
JP 2002017376-A/280
22-JAN-2000
07-JUL-2000
JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
                                                                                                                                                                                                                                                                                                                                                 PC
C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism='Homo sapiens (human)'.
Location/Qualifiers
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Secretory protein or membrane protein
FH Key Location/Qualifiers
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Pred. No. 7.3e-108;
0; Mismatches 12;
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Patent: JP 2002017376-A 280 22-JAN-2002;
HELIX RESEARCH INSTITUTE
 750 bp DNA protein or membrane protein.
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/db_xref="taxon:9606"
                                             BD123771.1 GI:23218716
JP 2002017376-A/280.
Homo sapiens (human)
Homo sapiens
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ilarity 96.9%;
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KOJI HAYASHI
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                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hayashi,K.
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Pred. No. 7.3e-108;
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Patent: EP 1067182-A 453 10-JAN-2001;
Helix Research Institute (JP)
Location/Qualifiers

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    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

750 bp | 453 from Patent EP1067182.
                                             AX136531.1 GI:14272935
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Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and HRI.
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                                                                                                                                 538 GATGITIGGACTGICACTGAGCCAGGCACGCCTGACCCCAGGGAATGCCACGCCTCCCAAAGG
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                         GATGTTGGACTGTCACTGAGCCAGCAGCCCTGACCCCAGGGAATGCCACGCCTCCC-AGG
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Homo sapiens cDNA FLJ32147 fis, clone PLACE5000116.
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oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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Isogai,T., Otsuki,T. and Sugiyama,T.
Direct Submission
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NEDO human cDNA sequencing project
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (basea 1 to 2783)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Riausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninch, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
Morkernan, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, B., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.
Butfeston, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Chenerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Squancing Dy: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (25-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 43 Row: c Column: 10.
                               Homo sapiens thrombospondin, type I, domain containing 3, mRNA (CDNA clone IMAGE:3844836), partial cds.
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: ATC
            mRNA
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Strausberg, R.
Direct Submission
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                                                                                                                                                                                                                PAT 03-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 GGTCTCAGCCTCCCCAGATCCTAGGCCTCTGAAGGAAGAGGAGGAGGCACCACTGCTCCC 200
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: WO 02068579-A 5949 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                          CQ720015 1698 bp DNA Sequence 5949 from Patent WO02068579. CQ720015 GI:42280872
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UM Multimegabase Sequencing Group.

Direct Submission

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Space (27-D598) Department of Molecular Biotechnology, Box Sipply Submission

Direct State (27-D598) Department of Molecular Biotechnology, Box Sequencing methodology, Mashington replaced gi:4186181.

Sequencing methodology: high redundancy shotgun with plasmids.

Interspersed Repeats were identified with RepeatMasker (available from http://ftp.genome.washington.edu/RM/RepeatMasker.html).
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14
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1775. 2058
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complement(6715
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                                                                                                                                     /product="THSD3 protein"
/protein_id="AAH33140.1"
/bx xref="C1:21619880"
/db_xref="LocusID:145501"
/translation="RPRLKEEEEAPLLPRTHLQAEPHQHGCWTVTEPAAMTPGNATPP
RTPEVTPLRLELQKLPGLANTTLSTPNPDTQASASADPRPLREEEEARLLPRTHLQAE
                                                                                                                                                                                                                                                                                                           LHQHGCWTVTEPÄALTPGNATPPRTQEVTPÄLLELQKLPELVHATLSTPNPDNQVTIK
VPEDPQAEVAS IDLLARESPNPPODTLESNLAALWAS FLWGDYKGERCNAFOEKGERKEB
VEDYPSEDIEGEDQEDEKEEDEREQALWFNGTTDNWDGWLAPGDWVPKDSVSYDYEPQ
KEWSPWSPCSGNCSTGKQQRTRPCGYGCTATETRTCDLPSCPGTEDKDTLGLPSEEWK
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DEHQCRSFRWRDASGPRERLDIYQPTARFCLRSMLSGESSTLAAQHCCYDEDSRLLTR
GKGAGMPNLISTDFSPKLHFKFDTTPWILCKGDWSRLHAVLPPNNGRACTDNPLEEEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 AATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTGCTGGAGCTGCAGAAGCTG 420
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Multimegabase Sequencing Group.
Complete sequence of the gene for serine palmitoyltransferase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GCCACCCTCCCAGGACCCCAGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCG
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Homo sapiens serine palmitoyl transferase, subunit II gene,
complete cds; and unknown genes.
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                          'db_xref="LocusID:145501"
note="synonym: TAIL1"
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                                                                            EST contigs that includes AA397580, AI138314, AA39545, AA868184, all from testis. The closest match in BLASTX is to E. coli pyrroline-5-carboxylate reductase."
                                                                                                                                                                                                                                                                               /rpt_family="Alusx"
12746. 12920
/rpt_family="BC200"
11921. 13217
/rpt_family="BC200"
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/rpt_family="AluSx"
complement (18624. .18771)
/rpt_family="LiMB3"
complement (18765. .18847)
/rpt_family="Li"
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14795...14857
complement(14844...14905)
/rpt_family="Alustrich"
complement(15106...15393)
/rpt_family="Alusx"
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ement (101)
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complement(19503. .20417)
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rpt_family="L1ME2"
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rpt family="L1MB2"
7883. .18175
                                                /product="unknown"
/protein_id="AAD09625.1"
/db_xref="GI:4186186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       omplement(15835. .16131)
rpt_family="AluSc"
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rpt_family="AluY"
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complement(20104. .20625)
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omplement(18244..18
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13236. 13751
/rpt_family="L1ME1"
13783. 14084
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/rpt_family="AluJo"
17778. .17804
/rpt_family="(CA)n"
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14085. .14403
/rpt_family="L1ME2"
14405. .14717
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                                                                                                                                                                                                                                                                                                                                                                                                                         57.9%; Score 370; DB 9; Length 231464;
81.0%; Pred. No. 1.5e-70;
tive 0; Mismatches 5; Indels 111;
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family="AluJb"
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Matches 494; Conservative
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PAT 20-JAN-2004
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human hela cells or other human
cervical epithelialcells
Patent: WO 0157278-A 165 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 CAGGACCCCAGAGGTTACTCCGTTGCGGCTGGAGCTGCAGAAGCTGCCGGGATTGGCCAA
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437 ACATGGATGCTGGACTGTCACTGAGCCAGCATGACCCCAGGAACGCCACCCTCC
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/organism="Homo sapiens"
/orl_type="unassigned DNA"
/db xref="taxon:9606"
/note="MAP TO AP111168.2~EXPRESSED IN HELA, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels 111;
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Pred. No. 1e-46;
0; Mismatches
                                                                                                                                                                               DNA
                                                                                                                                                                              497 bp Di
WO0157278.
                                                                                                                                                                              CQ064365
Sequence 165 from Patent
CQ064365
                                                                                         540 CCAGGAGGTTACTCCCT 556
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Best Local Simil
Matches 384; (
                                       480
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CQ064365/c
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KEYWORDS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human breast and hbl 100 cells
Patent: WO 0157270-A 161 09-AUG-2001;
                              GCAGCCCTGACCCCCAGGGAATGCCACGCCTCCCAGGACCCCAGGAGGTTACTCCCTTGCTG
                                                                                                                                CTGGAGCTGCAGAAGCTGCCAGAATTGGTCCACGCAACCTTGAGTACCCCTAACCCTGAT
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               CCCAGAACCCACCTGCAGGCAGAGCTACACCAACATGGATGTTGGACTGTCACTGAGCCA
                                                               GCAGCCCTGACCCCAGGGAATGCCACGCCTCCCAGGACCCAGGAGGTTACTCCCTTGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="texon:9606"
/note="MAP TO AF111168.2~EXPRESSED IN HBL100, SIGNAL
/note="MAP TO AF111168.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111;
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                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                    497 bp 1
Sequence 161 from Patent W00157270.
CQ049341
                                                                                                                                                                                                                                                                                                                                                                                                                                       Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                              CQ049341.1 GI:41023818
                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .497
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384; Conserv
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Matches 38
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                               RESULT 12
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PAT 21-JAN-2004
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                                                                                                                                                                         Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.

Human genome-derived single exon nucleic acid probes useful
analyais of gene expression in human bone marrow
Patent: WO 0157276-A 163 09-AUG-2001;
Aeomica. Inc. (US)
Location/Qualifiers
                                                                                                                  Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                   Length 497;
                                linear
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/nofe="Map TO AF111168.2~EXPRESSED IN
= 0.92"
                                                                                                                                                                                                                                                                                                                                                                                  Score 261.8; DB 6;
Pred. No. 1e-46;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 CACAACCTTGAGTACCCCTAACCCTGATACC-----
                                DNA
                              CQ130141 497 bp Sequence 163 from Patent WO0157276.
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                                                           CQ130141
CQ130141.1 GI:41087497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGAGGTTACTCCCT 556
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Best Local Similarity 77.3%;
Matches 384; Conservative 0
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                                                                                                    Homo sapiens (human)
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SOURCE
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RESULT 15
CQ130141/C
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                                                                                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AF111168.2~EXPRESSED IN PLACENTA, SIGNAL
                                                                                                                                                                                                                                                              Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R. Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta Patent: WO 015/272-A 166 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1e-46;
0; Mismatches
                                                                                                                   DNA
                                                                                                          Sequence 166 from Patent WO0157272.
CQ091307.
CQ091307.1 GI:41060168
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Location/Qualifiers
                556
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Best Local Similarity 77.3%;
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Homo sapiens (human)
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